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(54) Title: **CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI**

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon
5 programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp.,
10 *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal
15 infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of
20 unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is
25 thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism.
30 These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicide in response to specific
35 signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To

survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a
5 similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

10 Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

15 It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

20 It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

25 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

30 It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

35 It is also an aim of the invention to provide probes and primers derived from the nucleic acid sequences of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the Pathways™ software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

- preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473 .

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).
- According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence
5 to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined
10 nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of
15 at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
5 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative
25 amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant)
30 nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as
35 proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may
5 also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections
10 caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

15 According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the
20 invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a
25 compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively
35 monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for
5 altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing
10 and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays
15 will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
20 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
5 and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungistatic
10 compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or
15 underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which comprises
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

5 The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

20 The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

25 The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

30 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

35 According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

- 5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

- 10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a
- 20 downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was
5 used for the construction and the amplification of plasmids. Yeast strains were grown
under normal conditions on standard media (Sherman *et al.*, 1979). The
Saccharomyces cerevisiae strain INVSc1 (Invitrogen®) was transformed by means of
the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax,
after linearisation in the Ty δ element (Zhu, 1986).

10

Cloning of mouse BAX cDNA

Mouse Bax cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA
polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18
thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15 5'-ATGGACGGGTCCGGGAGCAG-3' and
5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to
standard procedures (Sambrook J. *et al.*, 1989).

20 **Plasmid constructions**

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII* GAL1
promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP
terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that
25 the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent
insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-
openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse Bax cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII*
30 and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final
expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture
collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results**Induction of Bax-expression in yeast cells**

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax
35 revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YIpUTyLMuBax and the yeast cells containing YIpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YIpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YIpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 · 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α-³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α-³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 µl RNase Block (40 units/µl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
- 10 µl α-³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid
5 scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the
10 detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP
15 labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during
20 prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating.
25 Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from
30 Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1).

Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; 5 Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to 10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally 15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test 20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti- 25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6. Assay for High Throughput screening for drugs**

35 $35\ \mu\text{l}$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers $2.5\ \mu\text{l}$ of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with $20\text{ }\mu\text{g/ml}$ uridine. A single colony is scooped
5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 μl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
- 5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),
- for the preparation of a medicament for treating diseases associated with yeast or fungi.
2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- 30 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

- 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 5 (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; and,
- 15 (d) a functional fragment of any of said proteins as defined in a) to c)
25. An expression vector comprising a nucleic acid sequence according to any of claims 17 to 23 .
- 20 26. An expression vector according to claim 25 which comprises an inducible promoter.
27. An expression vector according to claim 25 or 26 which comprises a sequence encoding a reporter molecule.
- 25 28. A host cell transformed, transfected or infected with the vector of any of claims 25 to 27.
29. A nucleic acid molecule according to any of claims 17 to 23 for use as a 30 medicament.
30. A polypeptide according to claim 24 for use as a medicament.
31. An antibody capable of specifically binding to a polypeptide according to 35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10

35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

15

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.

20

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

25

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30

39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35

40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20
25

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
30

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
35

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

15

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACGTCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTGTAGG
GACGTTTCGATACCAAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATCACTATTACTGGATTCAACAACGTATTCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVSGSTQACLPGVGRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAAGATTATTGGTTTTTC
CTAACCGCCGCGCCGCGCAGGTACCCCGCGCATCTCTTCTTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTAAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTAACTGTC
ATAGACGCATTTTGTATTATACAAATTAAGAATAAATAAATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTTATGGCTCTGTTGGATG
GTATCGGTTTCACTTACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTCAGAGAG
TCAAGAAGTATGAAAATGGGTTTATTAACAACCCCTATAGTGATTTCTCCAATACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTTACTCGTTCAGGATGTATGACCAAAAACCCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATTTCTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC
AGAAGTACCAATTAGCGTCCAATCTGCCAACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCAATATTGGATTCCCTCTCAAGGTAACCTCTATTTTCCAATTGAACATGATCAAAATGGA
TTAAAGAAACTTTCCCAGATTGGAAATCATTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCTPEDQADMVRRVKNYENG
FINNPIVISPTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQNSIFQLNMIKWIKETFPD
LEIIAGNVVTKAQANLIAAGADGLRIGMGTSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFSGSWFFYCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCAGTTCCTTCCAGATTATTCTAGAGATTATAGGGGTAGGACCGGAACGTGCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCCTTTTAGCGTATGATTCTTTTAAAGAATCTGGTCTTCTTCCTTCTATTT
TGATTGGGTATATTTCTATTCTGTGTTTCATTACTGGTCTGGGTAAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTCATTGTGGTATTTTATCTTATCGATTT
ATACTTTTTTTTTATTCAAAGAAAATTAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTAA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLVWVNWVLWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVFPM

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGTCTGCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTCTCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAAGGCAGCCTTTTACGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCCTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAAAACGGAAACTGGTG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTTAAAAACATTCCGT
TTGCTATTTAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCTTCTCTT
ATGCCCTTCAATTACCACTTTGATAACGGTATTTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGAAGAACACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAAATGAGTGGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC
CACCCCAACAACCTGGACTTCAATGACCTTGACACTTTTGGAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTAAACAATCTTCCAACAGCAATACTATTAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAAATTTCTT
CACAGGGACAATTTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTCGCGAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCACTCAGCTGCGCAACAACAACAATCTTTTTAAGACAACAAGTACTTTAACACCATT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTAACAATCAATTCCGTAAATCCCT
TACTGAGAAATTTCTCAATTTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATAACC
AAAATGCTTCATTTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQSSIETRDAIDKENGVTETGENSAKNA
EQNVSSTNLNNAPTNGALDDVIPNAIVIKNIPFAIKKEQLLDIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKMLPQAERERIEREKREKR
GQLEEQRHSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFKDKREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLQAHAAAAANSISNQAV
NNSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIIHSSQYNSA
DQPQQPQPQTQQNVQSAAQQQQSFLRQQATLTPSSRIPSGYSANHYQINSVNPLLRNSQI
SPENSQIPINSQTL SQAQPPAQSQQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLS AHNLSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC
CAATTAATTTGGCAGCCAGCTGACGATGTCATTATTCCCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAACCCCTATTTAAGATTACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTATCTTATTTATATCTCATCTCGTACGAAGGGCCGCTCATTTGGA
TCATTTTCTTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATATGAAAAATGCA
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTTCC
CTATCCTTGCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCTGTTTCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAATCCAATCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCCTTCCCTCAGGTTCTCCAATTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAATTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAATGGCTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTGTCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACCAGCTATGCCATTATTGCCTTCGCCGCATGCAAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCTGCTGACTAGGTATCTGCCGATTTTTCTTATTTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTTCGCAAGCTTTGTTAATATTGTGCATTT
GGCCTTTGCCTAACC AAAAGTCTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACATTTGTTGGGCGAGTATCCTTGGTTTGGCACC AACTTCACAGACAGACTATT
TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAATGATAAAAGGAACAAGAAAGACGAGCCGCACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTTAGAAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTTGT
CTCATATCATTTGGTTCTTCCACTTCCAGTCTTGATGGTTTTATTGGAACCAAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTCTTTATGTTAAATTAAGTGTCTGTTGTTTTG
CATTCCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAAACACACCAATTAATTGAAC
TGCCATTTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCCTGACAAATATTTTGATTTCAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTGAGAATGATAATTTTCGA
GAACTGCAAGTATGTTAGAAAACTGAACCTTCGTACTGATCATGCATCCAGAACTTTTGTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTTACGAGGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAAGAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAACTGTAACAAAAACAACACCAAGTGAACCACTGTTACCA
CTTTAGTTCCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTCATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTCCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDSDQDQDFSSAHMKRQPEQQQLQQHQFSPKKQRISHHDDSHQINHRPVTSCTHC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPTIIPNDSSPSSGPTSSAAQRDSKVSQ
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSESLEPPALQMAFYKNNAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT
SHVATNNNADRKTTPVATTTTMTPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSOLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWI RTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSDNNND
KRNKKDEPHVESKYKLPGSFRLLSLANFQAKLSHIIGSSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKIVT
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNQ
LTAWATSVENDISRTASMLEKLNFLIMHPEVFVEEDGII SRMRSHLTGSLFYDLVWCVH
EARRREMDPEYNKQALEKAAKKRFSSNGIYNGTSSTGGITDRKLYPLPLYNHI SRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNRNLTDASNDISIPNSIYPVASVPASNPNPQSTKVDYYSNGPSVI
PDL SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVMTMNNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCATTTTCAAATTAAGTGTTC
AATTATGAAAAACAACCTCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGGGCGGCAAAAATATTTGGTATAATTATGGAAATACAAAAGGGGAACCAT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA
GGAAGGCGGAGTCCGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCTCTGCTG
ACCTTACCGTAGGGCAATTTGTTTTATGTTATAAGAAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGTTTTTTGTATGTCACCTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDLTPPTAALMSAIYQEHKDKDGFYVVTYSAGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTTCAAGCATTGCTTGATTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA
GTGGTATTTCAACAACCGGTTCTTTTACCCCTTATTCCTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAAAAACAGGTATCCAAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCATTTAACAGTCCATTTTTTGATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAATAACTATGCTGGCGCTCTTTATGATCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTCGAGTTT
CAGTTGATATTTGGACCATGACAACAACACGAGTTGAAAGTCGTGGTTCTGGTGCTA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCATAATTTGGTTTCTG
GTGAAATTCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFDININNEVDFAFNRLLEGGLRGYAPRRQLANTPAKDSTGKEVARPNYAG
ALYDPRDETLDWDFDNDLSLFP SGFGFPRSVAVPVDILDHDNNYELKVVVPGVSKKDDID
IEYHQNKQILVSGEIPSTLNEEKDKVKVKKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTTGTCCCTCTCGCGAGGACCATTGTTGCTTGCTA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCTTGTAAATTACCAAAATCTTC
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCCTA
CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACCGGAAGAGCTAAAAAAGAAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGTAC
CAAGTGATTAGATTCTCTCTTTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCAGCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA
ATGACGGTGGCAAAATACCAAATGCCTCTGTCTCAGCTGTTTCTACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCCTA
TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCTTGGCCCTCATCAGAGGGAAGGGGTGAAGTTTCATGTATGATTGCTTAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAACAC
TAATGAGTATAACTTTGATTGGACATTAATTAGGCAAACCTCCTTTTGCATCAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTGGACATTAAGCTCAAGGAATTCTCCTGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAACCTTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGAAGCTTCGCTTCTTTCAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAAACAGATACAACGAAGAATTGTTGGAAA
AGGGGGAAGAAAGGTCAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAGTACCTTCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCACTTCTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAACCT
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACCTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGTTACCAAGGAGAAGGTCGTCGTAGTGTCTAACTACACTCAAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTCAATCGGAATCCAGCCATAT
TTGGATTCTTGTGAGTGCAAAATCGGGAGGTGATAGGATTGAATCTAGTCGGTCGTTTCG
GACTTATTTTATTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTACAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCGTTACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCGGCGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPKPRRVGSNKYTQLK
PTATAVTTAPISKAKVTNVLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKH
KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSDSLFTLFLKAGSNEVQLDYELKE
NAEIRSAKEALSONMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYVPFVDVNKIDNPIVMNKNAAEVDVIVDPLLKGFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCVPTLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFKLVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRLKNG
ASKILNTLKSLLDIRRKLTLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKGEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIKRGTKKVVVVSNYTQTLDIENLMNMAGMSHCRLDGSIAPKQR
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIDEKILQRQLMKNSLSQKFLGDSEMRNKESNDDLFNKEDLKDLSV
HTDTKSNTHDLICSDGLGEEIEYPETNQOQNTVELRKRSTTTWTSALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDELFDDEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAACAGCACGAAGCATATTATTGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTCTCTTCTAGGGACGAAAA
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAACAAAAAGAT
TCCACCACATACATCAGTGTGAAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTGCAGCTATTATTGACTTCATTAAAGAAATAT
CCTTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAG

CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTCATTTTTGCAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCCACATACTCGCTGTTCCGCATCCTATGGACATTGTCAATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCCAAAAAAGCTAGTTTCGGTTATCATGTTGA
AGAAATGTTGTTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCAGC
TATATTGTTTTGCGTTGGAAATTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGCTCTTTTTGCGCTACTATCTTATTGTCACGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAATTTGTTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAATTTGTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA
ATGGACCAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAATTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAACCTGACGGTTGGTCTATGGAACCTCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAACTCCAATAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTTATTG
AGCATGTTAGTGTTGCTATTTTTCTTCTTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTCCTCCCTGAATTTAATTGCAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGTCCTGCGAATGAGAAGTGCACCAAGAACTCGGTGAGAAACAGCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAAATGATCCGCTCTCTT
TATCCTCAGCTCCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATTTCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTGCGG
GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTTGCTGTTACTGGTGGCGAAAATAACGAAAAATCCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAAATATTAAGCCTG
TTGTCAACGAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCTAAGACAACCGAATCCTCTTCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDELSDDLHKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNAKKSKEA
KNFVIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQYTDPNWGATFDLDANFKKLLQFGYLVMFSTIWLPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHWINIVLYAVFIEHVSVAIFFLSSILKSSHDDVANGIV

PKHVNVQNPPKQEVFEKIPSPFNSNNEKELVQRKGSANEKHLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTKEKRS
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATMNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTTAAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTCGAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAAATGCAGGTACCATTCCCTTAGGCCAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTCCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGTTGAAAGATAACCCTACTGTCACTTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTTGTCATTTCTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTTGAAATGGAAACCACTTTTGCCAACTCGGACG
ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGAATCTTTGG
CTCAATACGGTTACATGGTGCAGAAACCAACCAAGTTTCGCCGTTTTTACCTCTAATCTTA
AGAGATGTCATGACACTGCTCAATATTTCAATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGCAGACTGTCAGTGAAGCTGAATCCGCTGGTGCCAACTTTGAGTGCTTGTAAC
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACCTTGACCTCAA
CTGACGCTAGTACTTTTATTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG
ATGTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTGCGTTCCAACCTTGT
TCAATGCCTCAGTCAAATTATTAAGCAAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTACCCACGATACCGATATCCTAAACTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAACTGCCGAATACGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGT
ACGTTCCCTCAAGGTGCTCGTGTCTACACCGAAAAATTCCAATGTTCTAACGACACCTACG
TCAGATACGTCATTAAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGTCTGTAAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGG
ACTGGAACACTACTCATTAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPHYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLSTDASTLFSWCAFEVNAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDITDILNFLTLAGIIDDKNLTA
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTGAGAAAAATATACATGTATCTTTTTCAGTTAATTTTATTAA
AAATAAATTATTTCTTACTTTTTTTTCTACAGTTTGCACCATTAACCTCTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTGCTGTTTTTTTTCAGTGTCTCGG
GCATACAGGCCGCTTATCTTCATGCCGCCCCATCATCTTAGGAACTCTTTTCGGTATGGG
CCAAGGGCAGGCGAAAATCCTATGTGCGTGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCAGCGCTAACC GGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACATATAATAAAAATTCTCAAGAACACGTTGTTTAAACGAGATAATTCCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTGTTGGAATTTGTCGATATTGGCTTCGGACAACCTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAAGACCTTC
GAAATTGATGATGAACACCGTATTCTGTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGTATGAATTCAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAAACAGGTTTCCCAATGAAGCAAGGTGTTTGTGTTGCCAAGTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAGAAAAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTGCGCTGCTTGGCTTTGGTCATTGTCAAGAAG
GGTGAACAAGATTGGAAGGTCTAAGTACGACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAACCAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCTGTGATTTC
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAAGAGACACCAAGAGCTTTGAAGGTCAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNI SYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD L AVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDV R DFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHRQALKVRNAQAQREAAA EYAQLLAKRLSERKAEKAEIRKR RASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTGCGACCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTGTTTGTGC
AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAACCGCTTCCACGGGACATGGGTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTTGTGTTTTTCAAAAATCTCTGGGTGTTTGTATGCCACTATA
TTTCTATTGCTATTTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA
ACGTCACCTTGGCTTGATATACTCGACGCTTTATTCTGCAAATTCAGGTCTCAAATCTGAA
CGGCGTGAGGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCACATCAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAAACTCTTGTTAGTAAAAAGAAAGGGAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GACTAACCACTATGAATACCAACAACAGTATAGCTAAATTTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAACTAC
TCATTACTCTTTGTTCTTTATTATTCTGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLL VKKKGKLVIWRHIVKKMLHIRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRVSRRRRKKREAERRDYD TYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCTATGCGTATGACAAAAGA
GCACCACGATGGTGTATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATACACCACTTAAGGTTTAAGTCATTGGACAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTTCTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGTGTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTGCGCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCTTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTCAATC
CATACACAAGAGAAATCATTGAAACAGTGCTGAATAAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFakteSEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGTSKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSLEFPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWDLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAATAAT
GACCTTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCGAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAACTACTTCTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAATAATTTACCGCGTTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA
AAAAATTGATAGAAAATGGATTCCAGACTAGATTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAAAATTACCTACAAACCAAGCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTACGTCTACAACACTACGGAAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTCGACTTTAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTCATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCCTTGATGA
ATGTTGTGCAAAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTGTCGC
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAAGCTTGCCTTGCAGTTGAACTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAAGTGTCTTTCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCATAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVPVPTYPTDAYIPTYLPPDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT

NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDFKRLKPLGMGKKRKRDSLSLPLNLQQPEYNDQDSTMGDNDNGEDED
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDVYYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTTIDLSKD
TTYGATTLDDVDVSHILHQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAACGAAAAATATATTTTTC
GCGTCGCGTCTCTCGCTCTGTTTTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGACATCCACGGC
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTTCTTCCT
CTAACTGTGCACGAGGCACCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGACTGTCTATTGGACTTTGCTGCGAGCTTAGACGACTTGTCCTTTTGGGCATCTCTGA
GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTGAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLSFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCCTTCAGCCGCTTTTGTGCTGTGTATTTCAGTATATCCATCATCA
TTTTACCTACAAGGAACCTTTTTATAGCCACCCTAAGTAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCCCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAATTAGGTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAAGACAAGATAATGACTACGACGGTACCCAAGATATTGCGGTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA
CGAGAGAGGCCCTTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTAACCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACCTC
CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCGGTCAAACCTCCGATGTTTCG
ACTTGTTCCCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGCCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAATTTGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTCTGTATCATGGTTTGTGTGACG
ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVHQAQDGLAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF
ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTPKVYHIDESLIDDPQECVDNYEKLIR
GFAGRDSVKLPMFDLFLGCPDGHIALFPNFQDNLREKLAWVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWSFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTTCGCTCTTAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTCTGAAGGCTTTATAGATCCCAAATACTACGCCCTTGAGAAATTGAAT
GCACTAGCAGTAATAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAGCA
TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACTTCTTGACGG
TAGAGATAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGCGAAGAAATTAATGAAATAAAACAGAAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTGCGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAAGTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCTCGGTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNRILSITLLLLLFFVFAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGGNEEIKKLHTQGLLESLLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAAATCCAGCTTCTTTTCAAGCAATATTGTCAAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTACAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTGTA
TCGCGATGTTTGAAGTGAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
GAAGCAATGTGATTCTCTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAACTTTTGAAGTGGATGAGTGCTCG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAGAAAAAATAAAGCGAACTCAATCAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGAGATTGAAATTGTCATCGATGGCCCTCTAAGGAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAGAGAGCGTTGGAGAGATAAAAAATTGGTTGATGCTTTTATAT
CTGAATTTGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGAAG
ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTTACCCAACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAATAATCTCGGATTTGTTGTGAACCCAT
GTAATAGGTTAGATAGGCTTACAAGTGATTAATGTTTTTGGCAAAAACTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAAG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAACTCTAAAACCTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAAACAGAATCAGCTACGACGGTAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCATATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNRLRLNFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEKRLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKIVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVPNCNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLIPERLALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLNGKGGQADFIDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAACAGGAAATGTATGGGTACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
CTGATATTCAGAAAAAACACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAACTGAATTTTCTTAGGTTGTGCGTCCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCTCTCTGTTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTCGTTCGGCCAGGCCGCTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTTTATTTAGCAGTGTTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA
GAACAACGGATCACCATTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT
GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGCGGTCTT
ATTTATTTCTATTCGCTCCCTTTGCAATGAATTTTGAACAGAATGCTCCAAAGGAGGAAGTGC
CAGGGTACCTCACTTGTTTACCCCTTTTACACAGTTTCAATAATTTTTTGAGGATTTTGAA
TTTCTGTTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAGGCCGTAAGGGTTTGATTA
AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACCTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCGGTTAATTTCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGCTACAGAACCTGAAAAGTACAAAAGGAGGTACATAAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGGAATCGTTACAGAATATTCCTTGAGAAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGAATGTGA
TGTGTGTTGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTTAAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCTAAGTACCATTGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCTTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIEKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPDEFLTDAMPIAKRLAKAMKLDYTNVLQNNKGIAHQEVDHVHFHLI
PKRDEKSLIVGWP AQETDFDKLGLKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAAATGCTTTCTTTATTTACGACGGTTACCACACCCGTACACCTTATCTCATTTTC
ACCACTACCTTTCTTATTTAGATTCATCTTATTTTATTTTAGGATTTTATAGGTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTCGCGAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATGTTTCACCTTCTC
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTCTATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRKRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTTCTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATCTATAATA
TTGCATCTGTGGTTTGCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTGCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAGTCTCCTTTAATGTCTGCAGGATAAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACATT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACCTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAAGCAAAATCGCTTTCCCAAAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKQYQPKDLRAKKTALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGTATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTC
CAGATACCCCCAAGGATCAATGTCGCAATGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATATAGTATGCCATTATGGGACCAATTTTACCAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATAATTGGAAGTTTCAATCCCAACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAGGACAACGGATATATTAATACAATTGC
ACAAAAAGTGTACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTGAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGAACATGTCCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTCAAAGACGTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG
CTAACACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTGCGCGATAATTATAG
CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATTA
ACAATAACAATAATAATTAACAATATGACCAATAATAGATATAACATTAATAACAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCGAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTCCACGTGCACGTATCATA
ACTTTGCTAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAACCAATCATTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTGCACCCGATGGGA
ACGATAACAAAGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAAACGAGTTCAAAGTG
ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCCGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVVLQVAHLPTPKDQCRIANIAFQIVNAETLVCHYGNTSLPSIEVNGTTKSLESA
MVQLDKDIHVDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHPILGQKKAISNNNCNTKSISINAANKTKDLDEIVRILEVSIPTTEAGSVPEIY
SLLKRTDILILHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTTQS
ELESWFTQYGVPRVGFVTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN
CPSCGF SNFRRRTACFRCSFPAPSNSQIHTANSNNNVNSSRNLLNNRVNSGSSSNI SNTA
ANHYPGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSP I I IADHFSGN
NNIAPNYRYNNNINNNNNNINNMNTNRYNINNNINGNGNGNGNNSNNNNNNHNNHNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGCGSNMPFRAGDWKCSTCTYHNFKNVV
CLRCCGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNDNKGDR

ISLMEFMSPLSMATKSMKEGDGNGSSFNFEKSDKANVNF SNVGDNSAFNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAACTAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCCTGAGCGTTTCGAAAAATTAGAC
TGACTTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTTCCACGCGCTCTCGATCAATGAACTCTTAAAAGTAACTG
ACCCCTAACTTTTTCCAGGCAAGGCTGGCCTCATTACCCTACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAACAAGACGAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRKRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTTCTCAAAAGATACTTTTAAAACCTAAAAC
ACAGAAATCATATTATGATAATTCAGAAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCACCTAACGGGC
GGGTTTGGGCAGGATTCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCTGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTTAGTGCAAGAAAGAGCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTTCGCAAGCAAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTTGCTGAAATTTAATAGGGAAGTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTTATTGTA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTTATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT
TGGAATATTATTTTCAATTTTTTATCCTATTAAATAGGCCGGTGTTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC
TTTCCCAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTTCCTTTAAAGGGATATATAACAGATTCTAAAAGTACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTGGGTGCGCGATATGTAGCTTGTT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAAAGTGTTTAATCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAAACAACCTTTTAAATGATGGAACTCCTACAGACAATATAGTTTCCCTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAAGCTCCCAACCAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAGATTCTCACCTTCTCCTATTT

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAATCCTTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCTTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT
TTTTGATTCCATAAGATTCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC
CTTATTCACCACCTCTTGCTCTCTTTTGGGTATCTCTATACACCTGTTGAAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAAATCAAATATACATTTTACATTACCCCTGGGGCACA
GAAGAAATCCGTCGGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAAACCAAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATCTTTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTCTTATTTGAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAATTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAAGATATAAAT
CTGACGAAAGCACAACCTGTACAGAAAATGGATATCAGGTATATTGAATCAGGATTTGTAT
TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACTTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTAATCAATCCTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAAATTGTTGTTTATAACAGTC
TAAAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTTGTTTTCGTTGATCGAAATAAT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTTCGACACAATTTTACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTTGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTTGATGAAC
TAGTCGAGCGCAGCTCCTGGACTTTTGTATTAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTTCGACCGATAATGAAC
TTGATAATAGTTTCAGGATCACTGTGCGGATGCTGAATCTACAACACTATTTCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTTAGAACTGTGCTTCTTCAGTACAGCCAGCTC
TGATTCTAATATAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAAATGAAA
ATGAAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCAATTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIIELEKPSTLSPLSRGKKWTEKLARFQR
SSAKKKRFPSPSPISSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPPKVAPFGYPIQRTSIKKSFLNASCTLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITFPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNTFFLHSPGLGHRRIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLLRVLVDKLMISKDGQR
YIQWCWFLFEDAFVIAEVDNDVDVLEIRLKNLEVFTPIANLRMTTLEASVLKCTLNKQHC
ADLSLDLYIVQNINSDESTTVQKWSGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHNDTVIIRRGFTLNSGECRSQSTVDSIQSVLTTISSIL
SLKREKPDNLAIILQIDFTKLKEEDSLIVVNSLKAITIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVDSKIDELVEASSWTFVLETLCYFSGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSMDMDKIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCTTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC
CTGATTTCAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACCTTCTTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATGACACGATGAAATCAATTTTAGTTACAATGCTGGAAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCCTTCTAAAAATA
AGGAATTA AAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAAGCTAGCTGAAGATG
GAAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAAGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTCTCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTTCCCG
ATGCTAAAGAAATCATCAATTCGTTTCAATAGTGTGAACTGATCCAATATGCTAAAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTGTTCATTTTATCA
GACAAGATGCAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGCTTGCCAATCCAAATGTCTTGGTTCCCTGCGGTTAACAAATTGATTGACTTGGCCGTCA
AGGTTTCTGATAATAACATTAAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCCCTGGATATTTTGAGAGTCTTGAATGCAGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTTCAAGCTTTTGAAGAAAGAGCTGCAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCCGCCAGTGGTATCATTTGCCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTCGTAACAGCGTAGGTGAAGTTCTTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACCTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTTTTAAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAC
TGTTTTAAATTCGAAAACGTTTCCAAGAACAAAACCTGTATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAACTTCTGGAGGTTGCATTCCTGGACACCA
CCAAATCCTCATTCAAGAGACAAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT
TAAAAGACAGTTGCAAAAACATCGAACCATTGATACGCCGATTTCTTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTTCAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTGTTTAAATCAAAACGAAAGAAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG
TGATTCTCATGGCTTCCACAAATTCACGTGTTACTGTCAAAGTTTCTCTGCTGACACAG
GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACACAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAAACAAAATATCGGTCAAATCAC
AACTACCAACATTCATGCTTATTGAGAGAACTGGTCAAGGGAACATAATATGGGTATTTC
TAACACCATCAGAGTCGTTGGGAGAAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTTCAAAA
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPEL
LMHIIRFVMPSPKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTRLRFLTKLREAELLEQMVPVSLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFQFIRQDANRT
PALKAQYIELLMELLSTTTSDDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELOTTVNNPDQDKAMQYRQLLIKTI RTVAVNFVEMAASVVSLLLDFIGDLNSVAASG
IAFIKEVIEKYPQLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTI IKLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSLVEKKIDEDSLERVMTSISILDEVNPEEKKEEVKLLLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDCKNIEPIDTPISFRQFAGVDSTNVQKDSIEEDLQLAMKGDH
ATSSSSISKLKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNVIPHGFKFTVTVKVSSADTGVIFGNI IYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRTMWNFAFEWENKISVKSQPLTHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCLNYAKSSFGEDALANLCIEKDSKTNADVIGYVRIRSKGQGLALSLGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT
ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAGGCAAATGTAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCTGTCTACTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGGCCCTGCTTCTTTTCCTTTTGATTTCTTTTTTTATCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTAAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGAAAAGCAATGCGAGTTGAGAGATTGTGGAGTGATC
TACAGAACCAATATTAAACACAATCTTTCCCTCAAACGTAAACACCGAGTTTTTTTCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCTGTCCTCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCTTATACATC
CATCTTATATATCCCTCCGCAATCTAAATGAAAGAAAACAATCAGCTTCTTACACAGAC
CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAACAGTGCTGATACCGCTAAAAATTGAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTTGATAAAGACACCCAAC
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATAC TAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAAATAAATACTTCAAATCATTAACGATTCATTAA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAATGAAACCTAAAACCTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAAGAACAACGAGATGAAATAGAGCAACTAAAAAATAAGATCCCTGGAGGAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDMYNQSSSMATYNASEKNLNEHPSPIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNP IQPPLPNLMHLSGPSDYRSMHQSPIHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKVPDPKDTQLISSGKTLRNRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFDDLAEENNFKSLNDSL RNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNM LKNENSI IKNEHNMSR NENENLKENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCAT'TATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCCTCT
CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC
TAACCATCAACGAATTAATAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTGTGATCTTTTGTTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATATGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTGGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAATGGAAGGAAGGAAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTTCCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT
CTATGGTTTAAAGAATGTTTAAAGCCCTTCTGATACAGGTTGTGGTACCACAACCTTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGTCGGTTCCG
CTCCAAACTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAAATAGCACAAA
AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCCCTTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTTCACACCAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGTCTATTGTCGTAGGTTGTTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAAACATTCAGACCTGAATATAATGGGCAACC
CTAGATATTCAAGTCATTTTCATTTCTTCAAAGACCTTGAACATACACGAACATATCTGACA
GGTTGTCTCAAGAAAGGCTGGCATTTCATGCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATTCTAAACCATCCCCAGACGGAACCTAGCGCTCTAT
ATGGTGTGCGCCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFPLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSGAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVVRKMESEVSMVLRMFNAPSDTGCGTTSSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPFHGIADDIEGLGKIAQKYKLPLHVDSCLSGSFIVSFMKAGYKN
LPLLDLFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPATWGGLYGSPTLA
GSRPGAIVVGWATMVNMGENGYYIESQEIIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNHELSDRLSKKGWHFNALQKPVLAHMAFTRLSAHVVDIEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTCTGT
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCCCTCAAAAGTATA
TATATTTAGAAGAGAGGAAATATTTTTCTCATGTCTTTTTTAAATCCCTTTGGGTGGCG
AAAAAAAAGAAATGTAAAAAATTTTGCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCCTCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAGCATTGCTTTTAAAA
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTCCTTTTCCACTACGAACCTTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGAGA
GTAACATTTGTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAATA
ATTACCATCCCTCAATGCAAAAACCTTTCACGTACGGTAACTTGCCATTGGTGATACGT
TAAAGCAATTAAATGAGCAGTTCAAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTGTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCCTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATTTTAAAGACACTGTAAATAATTTTTCAAAACCTGTTGGAAACAGAACATC
CTTTTGACCTCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTTCTATACTACCTGGTTGGACAAAACAAA
TCGATCCTTTTGAGAGCTTGTGTTTGAGGACGTTTTCGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTTCATAAACCTT
GTTTCACGTTTTCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATCTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCTTAACACCACAGAGCCTCGCC
TGATTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGAATTC
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTCTTAA
TCCGCTTAATAGCATCTTCAAAACACATCTTCTGTAGCAGATGCCGGTCATGCTGCAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGCAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTATACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAACATACTTTGATAAAATTTCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCATTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTGTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACACTCTTAGACGTATCTCTCCTGGACGTTT
ATAGAGTCGCGGAAAAATATCTACTAAACAAGAAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTACCAAAATTGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRLPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSANFMNAMTG
PDYTFEFPFSTNPDQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VYNNEMKGQISNANYFWSKFQSSIYPSLNNSGDPMKITDLRYGDLDDFHKKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSYQGRKRLDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDITYDTFLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFGL

QLLYSILPGWTKIDPFESLLFEDVLQRFRGDLETKGDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNMTSRITDTNGITYVRGKRLNDIIPFELFPYLPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE
TDFHKNSDKLKVLRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPHYTHKDGSAQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEGVTYFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCTT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCCATACAC
ATTTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTTCAAAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATCGTGTGGTATAGAGCTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTTTTGGGTTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTCACACACAAGAATCTTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTTGAGTCTGCTATTTTGGCTCTTGTGGTTTCGTGGCAAATTTGG
CGGCTAACGCTGCTTTGTCTGATACACAGTGGCTTCGTCAACAATCTTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGCCACCTAGTCTAGGAATAGAACTTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGTCTTTGTTTGAATATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCTTCTCTCTTTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTTGGGTACAGTGTCTATACAACCTTTTTGAAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTTCAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAAC
TCCACATTTCTTTTCTTGTCTATGTTAAATTGTATCATTATCTTTGTTAGTACTATTTTT
GCTGTAAGCCCTCATTTTGACATCACCTTTGGTGGTTACCGTTGCCTTAACCTTTTACTA
TCCCGTTAGCCATGTTCTGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTTATTTTCATTTTGTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISSEFALYLTP
DLWRIIQSRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLFLCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKLLGLFV
SLFGIILIVMQSSKQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLFWPILIIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFPTPWYIIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAAACCTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGCTCGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTTCTTGCAGGAGACGCGCTCAGGGGAAGTCCGATTCCGAAAG
ATGCCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGAGAGCAAAATGTCGCC
CCAGCCAGTCCGACACATCTGTCTATTCGACCACCTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTCCACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTT'TTACTAACGTTTATCAATAAGTTTCGGTTTC
CCGTCTAAATTTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGTTGGTCGTCGTTACTCCAACCTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTTATGCAAAACCCAACTCACTACAAAATCCCAGCTTGGTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTTCGCTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPTHYKI PAWFLNRQNDITDGKDYHTLANNVESKLRDRLERLKKIR
AHRGIRHFVGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCCGGTGTGATTTGTGTAACTAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCTTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTCTCCATTCTATCTATCACAAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTCTCTATG
TTTTTCAGCCATACAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAAGTTAACTTCCAGCTGCAAAATATTCAAAGAATTTGCAAAGATCAAACA
CAAGCAACCCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCACTAACAA
ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAAACAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCAGTTACTTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAAATAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVIVIGGSQDWLKHSLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNLFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQWSMTQAQLTNDNLQNTMITINALKQTNNAKQAQYKINIDKLQDMQDEMLDLIEQG
DELQEVLMNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEEPFLDTEKKNKALESQA

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAAATCAATTAAATTCCTTTTCTCTCTACCTTTGCTAATATTA AAAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCCTGTTAAGTTTCCTATTTTCACCTTGTTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCTTTTGTGGGTGAAGAGAAGTAGTATTTTGTTTTTTTCATGGGAGTGGAAGTCCTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTTGGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAAGCAGCAATATA

CACATTTAATGGTTT GCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTCAGGTGCATAA
GATGGGAAATTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAAGAGAGGGCCCCGGGGAGCACCACATT
CACGACCAATCGTGTCTGATCTGCAAAAAAGGCACATGGAAAATGTAATTTATCAGTGTTT
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAAAATATCATTAGAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTCTGTTCGTGGTCGTTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCCGGTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAAATCAAGCCATTCATCAAAGTCGTCAACTACAACCACTTATTGCCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVVRGRYAGKKVVIVKPHDEGSKSHPFGLVAGIERYPKSVTKKHGAK
KVAKRTRKIKPFIVVNYNHLPLTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACCGAT
GTTAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTAGTTAGGTTTACC
TTGAATTTTTTTAAAAAAGAGTCAGACAGGCTCGCTCTTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCCAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTC
CCGCTCTAGCCAAATCCGAGCGTTCATCGATTTTTTGGGGAAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAATCT
TTTGCAATTTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTCTTCAGATGACG
ATGATGATATTCTTTTGAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATCCCCTACTTTGGAGGTTACAACGACCACATTAA
ACAATAACAGAGTAAAAATGATAACCACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAAAATAAATTTTTGAACATTGAAAGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCACCGTCAACAACATTATCAACAA
ACACAAACACTATAACGCCAGATTTCGTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA
ACCCAAATAGGATTATTTCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTCTGTCATTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTGGCATGTAAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTCTGCTCCTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCCTCAGA
TTTTCCAATATGAACTGATAGACTATTTGATAATTTTCGTATTTCCTTTGATCTCCTAGAAG
GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAATTTATATGGAATTTTTTGGATGAAA
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATTTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA
ATGTGGATACTACAACCTCTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCCTATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTTAA
ATATTTTTGAAAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATTTCTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAAGACCATTTCAAACAATTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDILLELGTRPPRFTQIPSSAALQTQIPTTLEVTTLTNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKENIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTSLSTNTNTITPDSSSVAIEAKPOSPQSKRK
ISDNLKKNMVLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCCKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVPEQIFQYELI
DYLIISYSFDLLEGLRLVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMNVNIFS
AVEVUNIITSIIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTT
HMSKYHDFGLIRNIGDNELGGLISKLIYDRLQSVPRVISEDIGMDSDFKTAPIIGYK
MEKWLLKLDVLNIFENLLMIYGDDATIVNGEMLIHSSKFLSREQALMTERVVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHFQKQREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESFSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTTCCT
ACTATTACTAACTTGAACCTCACTTCACTGGAAGAAGCTGGGTTATTCAAGGTAAAGAAAT
CATTTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTTATTATTATTTCCCACTTTTTC
ATCGAAGGAAACGCGTCAAATCCATTCGTACTACGCGCAATCTGCGTTATTTCCCTTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCCTTTTGATGTTAAATTAA
AAGCGACTGAATGAAGTGCACACATTTTTTATTTCTTCTTGATTTTCTTTCTATTTTGT
TTTGCTTTCTCTCTGTGCGACAACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATGCCCCACTTTGATCAAGAAAGATATTCGCAGCACA
ATACAATAATAACATTCAAAATGGCAATCAAATGGTAACAGTATTCTGCCATAAAGGATA
ATACCATCGGTCCATGGAAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG
TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTAATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTATTATTTGTTGTCGTACTGTGTCATGCGTTGGGTATTGTC
ATCGTGATCTAAACCGGAAAATCTATTATTAGATCATAAATATAACATCAAGATTGTCAG
ATTTTGGTATGGCTGCTTTGGAAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCAATGCGGTGTGATCCTATTCGCCCCTTCTTACTGGTCGGTTACCTTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCCTT
CTGATGATGAAATTTGCGGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAAGC
AACAGCAAGTTAAGAAGAGGCAGTCAATTAAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG
TATCGACAACCTCCACAACGCAGAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCCTTCAAAAACCTTCTCTTCAAGAAGAAATATTCTA
CAATCGTTAAACCAATCTTCTCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAATCAAAAAGAGCCTCTATCTTTCTACTACCAAGAAGAACAAAAGAT
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGTCAACTTTTGATAGATGAAATTTTTGAGTACG
AAAAGTACGAACAAATAAGGAAAAGAGAAGGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGGAACCAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAGAAAATTTTAGAAAATATCAGAAGAT
CAAAATTTCTTGGGTTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTGAGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCCAACACCAAGAAAGTGCGGATGATT
CAGAAATTTCTTTTGAACCTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTCGAACG
ATGAGAGATTGTACGATGTGCGTGATTCCTATCAAGACAAATCCGCGTTAAAGCTGA
ACTTGTGAGATCGTTTAAATGGATCGAACGGAACGAAACAACTGATAACTTACATCTTC
CGATCCTTCCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAAGAGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAAATTAGGGAAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAAAGATCAC
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAATGGTTCTTCTTTAGAAAAT
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTAGAGAAGCTGTTGCGTGTTGGACTCAGTATGGTTTAAAAAATATAAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTTATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINNSIPAIDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEA AVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYP SIRD SKS
IRGLPREDTYLTP LSESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANA EKTLYALL
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLISVTSRKKPISF
NKFTASASSSNLTTPGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYKEYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEEELKKQIEIDISDLEQELSKHKEEKLDGNIRSI SAPMENE EKNINHLEVDIDNIL
RRRNFSLQTRPVSR LDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVGSQ LKDDSTAT TAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKGNLDVNNQ
QSQRIPTR SADDSEFLFETVNEEA EYTGNSNDERLYDVGDSTIKDKSALKLN FADRFN
GSNEAKQTDNLHLPLPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSSTEKEEENE
EKEEKKPEQHKEEDQEKREKVDDMEPPLNKS VQKIREKNAGSQAKDHSKDLKEHKQD
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNNL T
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSV VQFKKVS GSFKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGTACTACCGCTTCGTATGCTTTCTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAA CTATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCTCAAACCGTTTTTTTGCAGTATGTTATTGATCCATCG
AATCAAAATTTTTTACC CGCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTTAAAAGGTTTTTAAAAGTAGTGTTTCAGCAGT
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCCAAAATATAACCAAGATAAAGAAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
ACAATTCAAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAATAATT
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAAACAACGTGTACATACTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTAAATCTATCGAAA
GTATCAAAAACCAAATTGAATTCTATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT
TAAGCTATAAATTCAAAAAGCCAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTACAAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCATCCATTGGAAAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLDNPNKNTSSAAEDKKKQTSCLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSNTKWTPITPSVIIISGSKDTNSKSGKNSKNSKTNKKMKKRGKYNNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKIRITMNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNSNRNSYKQLS
YFRQQQYNNINYYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCTGTTCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACTTTCTGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAAATATATA
TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTCAAAGGCACGCGTGTCCTTTTTTGTGTTAAGACAATAGATATTTTAGC
ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCCTGTTTGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC
TCGTCGAGTTTTTTGCTCCATGGTGGTTGTCATTCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCTCTATTTTAAAGGAGCATAACGTCCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTGTATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTGAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC
AACCATACTTGGAAAATGCAACTTTACCACTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTATCCCTTC
TAGATTGAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATCTGT
TTGATGGAATGTAGACTCTTTGGTCGGAAATTCGTTGCTCTAACTCAGTGGTTAAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT
CTACAATGTTTCCACACCACGTTAGATTCTCTAAATATGAGAGAACAGTTCCCATTTATTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTCAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTTCGCCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTACAGGGGCAAATGATATCTTAAGTTTCTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVATITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLPTNTTETPILFDGNVDSL VGNSVALTQWLKVVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPEKQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTGGAA
GAAATAGCTAATATTCTGTTATTTATGCCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTGGAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT
TATTAGAATCGGGAAGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AAGTTGGCGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAGAAAGCTGCAAATTTCAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCTCAG
GCGTCATTCTCCAAGTGCTGATTTGGTGTGTTGATGTCGAATTGGTAGACGTGAAATCAG
CCGCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGIIKRIPVEDCLIKAMPGDKVKVHYTGSLLSGTV
FDSSYSRGSPIAFELGVGRVIKWDQGVAGMVCVGEKRKLQIPSSLAYGERGVPGVIPP
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCCAATGCCCATCGTATTGTACTCAATGGTGAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTCTAACGCA
TGCATCTGAGCAATGAAATCATGCAACCAATTTGAGGTTAATATATGAGAATTAACT
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTTCGCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAATAAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGTGCTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTTCAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACCTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTTCAGACAATGGTTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNLTAKAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGGGCCCCGTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATAACATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCCTGCTATGTGAAATGGCTGGCGTAGCATTGTACCAGGACA
GGCTCTTCTTACCCGCGCAGTTCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACGTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGACAGGAGA
TGGATACGCTACCAGGGCAGCCGCCATTAAAGCTGCGCGACTTCCCGCAATGACCAAGG
CTATGGGCATAGCATTTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTT
GGCATGTTCCCGGCCAGCGCAGGCGGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAACCTAGTGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQQTSSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPPRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGPPLRLRDFPQMTKAMGIALM
QQDEQAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCATTGACGTAGAAAT
TGAAAGAAGGAAAGGTATACGCAAGCATTAAATACAACCCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAACCTAGATCTACAGCCCCTGGAAAAATCGTTTGGTCAACTTTGAGGT
TCCGGTCTGTCCTTCTTCTGATCTGAAAGGTCTTCTCTAAATCTATATTAACGTATAA
ATAGGACGGTGAATTGCGTTCTACTTCTCAATTGCGTTTGTATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTGATAATCTCAAACAAACAACCTCAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAAGGATTCCGGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEQGESLADQARDYMGAASKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTTCGGCAGAGTCGTGGACACCTTGAAGACACCCT
TGTTGCTTCTCGGTTGAACCTTACCAGCGACCTTGTGCGCCTTGTGAGTGATGTTTCCT
TACCTTGTTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTGTTTGTGAGTTGT
TTGTTTGTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTTGTTGTGGGTTGTATTAATGCTTGGCTATACCTTTCCCTTCTTTCAATTTCTACGTC
ATGGGTTTTTTTTCCCTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTCTTACTACGTTTCT
ATGTTATTTTGTGCGCGCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTACCAGCTCTGGCTTTTGGCTTCTAGTCCTTGTCCTCAAGAG
CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTCCATTTTTCGGCTGGGCGGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGAATTTGCGCGTCCCTTTTTTTCTTCATTCTCTGACTCCCCCTACCTTCTCCCCT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAACTCCGAAAAATACCGAACCAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHCHYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCCTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTTCGTCACCATTTATCTTGTGCGGTGTTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA
AGATTAACTTACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTGTTTTAAAGTGCGTATAAACCCCTTTTGCTATTTTTCGTTTATATAAT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTTCGTCGTTGCTTTCATCGCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG
GTTTAAAGAGGGCAATCTGGCCTTGGCGGCAGTAGCTCATCAAGTAATATCTTGGGCACCTC
GCCAAAGAGCTCAGTCCACAAGTTCCTTGAAGTCTTTAAAGGGTCCCTCCTCACCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTCTTGAGAA
CCATTTACCCGCAGCAGTGGAGTTATCAGAACTGTTTGTGTAGATAACTCATGGCCCCG
CAAAAGTGATTATTCTATTTTCAGTACCCCAAAGCCGTAGCTATTGGTTTCAGCCACCC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAAATTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCAATCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAAATCCCGAACAGCTTATCAAACGTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTCCGCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG
TGGCACTTTTCAATAAAACCATTTGTCATCCTCGAATTTGTATTTCGCTTTTGTAGCACCATA
ACCAGAAAGACGAAAACATCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTTCACTCGCACGGCTGTGGAAACGTCGTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCAGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCCTCCTTCCCTACCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACCTTCGACAAACATTGTCAT
CTTCTATACCAACTAGCTTTTCATTCTCTAGTTTTATGAGTAGCACTGCTTCCCCATTTT
CCATAATTAAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACTTAATGAGT
TAACATTCGAAAACCTTGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLS SSPKIRKYNKVFN YAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGN YDPPFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLR TISPAAVELSETVCVDNSWDPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKV VLFENYQYCDFFPPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNVCVQDCDVR SNIKV
RHKLKFFIILINPDGHKSELRASLP IQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEYLF SRSASVTGLELLADMRSGGSVPTISDLMT PPNYEMHVYDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRILR LTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPADGTGERILPQSALGPNSGSVPGVSNVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYKAMKYDIIGEDLPSPYCAIQNVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSLNTLNLELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAACGTTCTTAGGATTGTGGTGGTAAACTTGTAATAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCCTG
GATTTACCTTGGCATTCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTGCGGTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAATAACATAAACTCACTAGCGGTGAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAATACTGTTTCGTATATTTTTTT
GTATTTCAAGAACAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCGGTTATAAATATGGTTATGATATGCCAT
GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTAGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACAA
AACAAACAGGAGATCACAACAACTTAGAAAACCATTTCAAAAAGAGTAAAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATTCT
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAASAAGYDRHITIFSPGRLYQVEYAFKATNQTNINSLAVRGKDCTVVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGKATATGPKQOEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTC
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAATGAATCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGCGAACGCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTTTTTTTCAAATATGTTTGAAAAACG
TGGATTAAATATAGTGATAAAATGAAGGTGAAATCGATTCTTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTGTTGTCGGTGCTGACTCCAAAATCTTCAGATTCCAAAAC
TCAAATCTGCCTCTTTGTTCAAGCAAAGAAAGAACCCAAAGAAGATCGCTTGACTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLKFQQRKNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLEKANKEKKKA
AARKAEKAKSAGTQSSKFSKQAKGAFQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTTATTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCA
GGATTACATTCGCACAATAGATAAATGACTAATTTTCAAGAATTTGTTTCAACCTGCCG
GCATTCAATTATTATAAGTTATTGTTTGATGGTAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTAAGTAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTTGACATGCAAGTTTAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTAGCACAGGAAGTGAACAATATATGCGAGCAATCCCCTCACCAACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGTCTAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSIFSIVASVLAQELTTICEQIPSPLESTPYSLSSTTTILANGKAMQGVFEYYK
SVTFVSNCGSHPTTSKGSPIQTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTGTTCTGTACCCCGCATTACACCGCTCTGCCTATTCATTTTATC
GTTTTCGTCTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTGTATATCCCTCTAACAAATTATTACAAGTGTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATTCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAACCTTACGGACCTTCTTTTGAAACGA

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTCATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAAGTACAG
TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACCTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCAGTCAGATGCCATGAAACAAGACAAGTACGTACGACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCCATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDFEVPTEKLLRETKVGVEVNFKKSTNVE
ISKLVKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLDRQVLKALYDLAKESEHPPQSILHTAKAIES
EMNKNVNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEETIAKQNLNAQGATIERSVTDRTFCGKCKEKKVSYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG
TTTTCAAAGTTGTATAATATTTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCAGATGTTAACTGCAGTCA
TTTTGTTTTCTTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTGTATTGTGTTTTCTTT
TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACCTTCAAAATAGACAAAGACGAAAAAACGGTGAAAATCGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTGTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTTCAGCCAACCTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATTTCTACCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCATAACTGGA
GCAGTTTCTTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAAATTTGTTCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTTCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDDNWNINWNSTLTQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFDQCPQFVQVDWLPMSLLLVEVSHTNLTEITWMVFIHVNSVVMILTGTHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCCTTTC
GAAAAACACAGCAAAAACAAGAGTACTGTAAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTTATTTTCTAATGCCTGTTATTTTCTTATTTTCTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTTCTCGCAGTTTTTTCGCTTGTTTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCTTCTCCGTTGATTTTTTCTCTTAGTGATTTTTTGCATTAAATCCCAGAAC
AATCATCCAACATAAAGAAATGCCTTCCAGATTCATAAGACTAGAAAACACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGTACTCAACATATTTCTTTGTGTTTTGATTGCCAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACCTTTCATTTAGAT
TATGGAAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAAATGTCCAGTTGAAAACCTGTTTACTAACGA
TTTAAAAATTGTATTTTATTACAATATTTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAAATACCATCCAGGTTATTTCCGTTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAAC'TTGGACAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTTCGTCTCCAAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKRHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
YFHKQQAHFVKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRI
PNVPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCCTGGTCTTAGCACCACCTTTTTTCCGCTATTGTATTGT
TGAACATAATTTAGTATCTATTTCCATTTTCATTATAATTCACGTTTTTAGCAGCCCTCTT
CTTCTAGGTAATTGGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTCGATGGCATTATTTT
TAGTCCTTTTGAAAGCAATATCATAAAATATATATAGTTCTCCATGATGTTCCGGTCA
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAAATACGAAT
CGACCGCTAATTTAACAATATGGTTTATAGCAATGGAAAGTAGAGTGGCACCAGCAATTC
CTGGGCTCATTTAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATAT
TGAATTCCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTACGATT
CTGATGTGGAAGAGAAGCTGCTTGCATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAAA
AGAAGAAAGAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAAACTAACCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTTCATTGTTATTTAAATGGAAGCCAGAACAAAGAA
ACACCGTGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAAGTTTGGAGAGTATCAACGATTTCAGTTTCAT
TGGAGGACCTCGAGGAAATTTGTTGGTGATATTAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTCCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

LAHDYVCEKTDGLRVLMFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGE LVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTPVKAPYTAGG
KDSL LLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRYNYNDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLN GNHSTSVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWS

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAGAGAGCATTTGGGCAGAGAGTATTTGTCTCGGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTCTCTCTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGAACATTTTTCATCCTTTCTC
ATTTTGTCAATTCATTTTCTGTGGAAAAATTCACGTGACGCGAAGAAGCGATGAAATTTT
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAACTGCG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATAATAGTATATTTT
ACACTCAATTCATTTTTTGTATATTAAATAGTGTGTAAAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG
AAGGTGTCACGTGTCAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAAGCTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCCTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATTTGCTTGTGTCAGGTAACCTGTGCGAAGACG
TTTCCCAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTCTCACAAGGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVFVRDGV TIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACTCGGAATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACCTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTAGGCGAAAAATAAAAAAATATAAGTAAA
GAAGGAAAAATTAGGCGATATTA AAAACAAATCTAAAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCA
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTCGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCTTTTGGGCAATTA AATGGGGTGCCTCAAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTC AAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGCAGATGAGTCAAATCTTTAACACTAAATTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCCCGTTGTACAATTTGAATCTCAGCATTTCTATGATTAATAATTCGA
ATTCCATCAGATCGGTGAAATTTTCTCCTCAAGGATCCTTATTAGCCATTGCTCAGCAT
CAAATTCATTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTGAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTTTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLSDMK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFHFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRSVM
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLSVPTHSSQASLGEFAHSSWMSLSFN
DSGETLCSAGWDGKLRFWDVKTKERITTLNMHCDDIEIEDILAVDEHGDLSLAEPGVFDV
KFLKKGWRSGMGADLNLCCVCLDRSIRWFRAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCGAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCTTTGATGGTCGTGTCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAAGCAATCCAGTT
GCTTCGTGGGTTCGACTGACACGGTTTCATTCAGAAACTCATAGGGACAGGCAACGCAT
CTCCCTTCGGACCTCCAGAGCGCTGAAATCAATGGATTCCCTTGGCCAGCCTAGCCGGAG
TGCCCTGTTTTCAACGCCCTAACTGAAAGCCACCTCATTTTGTAGAGTATTGTGATCC
CATATGTTGGCTGCTCGCCAATTCTTCCTGCTGCAATACGCTTGTCGCCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTCCGAAAGTTCCC
TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCTTGCTTCTGTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCCA
TCAGCCCATTCGAGAGCGTCGATTTCCTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTTCGACGAACACTTACCAATATCTGTTAACGATGGTGTAATGAGAGTAGTATGCG
CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTGTCTTGGTTGTGGGTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNSLSIWALGPHTAGPLLLFS
ILNCTPARSVTLPISPSRASISFTRMPLTPPIEGLHEHLPISVNDGVMRVVCAPVLDDA
AAASQPACAPAMTTTCVLVVGWKLKEDMVNRLRLRTCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTTCTGGTCACCTGGTCTGGGGCAATACCAGTCAACATG
TGGTGAAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCGTCAGACTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATACAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTTCGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTTGTCTTGAACGAATCATACATCTTTT
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTTCGTATGCGCAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCTTTTCTGTGCCTGTGA
CATTTCTTTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTTGGACCTCGTACAGAAG
CTTATTGTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLPRTAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTTCCT
GTGTAGCCTAATGTTTAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCATACATTACTTTTTTTAATATTCTTTTGTGTTT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAAACTTGGACATACTCATCATTAAAGAAGTATAGTTAAGA
GAGGCATTCATTTTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGCTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTRFGIR
RNEKIAVHVTVRGPKEEILRGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCGTGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTTGCCATTCTTATACATTTTCTTTCCTTCTGAAATTAACCTGTACACCCA
TACCTTATATACACCCATACCCATTTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCCCTTCATCTCTGCGGATTGCTGACGGAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAATAAACAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAAGCTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAAAAAAACTATC
AACCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAATAAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTCAAGTCTTCTCCATTGCTGGTCTCTC
TCATGCCAAGGGTATCGTCTTGGAAAAATTTGGGTATCGAATCCAAGCAACCTAAGCTCTGC
TATCAGAAAGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT
TCCAAACGATGGTTGTTTGAAGTTTGTGACGAAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGTTGGCTTTGTGGAAGAAAAAGGAAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTACGCCGTATTTTTCTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTCTAGAAAGTTCCGGAAATTCG
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTTCCGAACA
GGTCGGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTCATAGAAGCCTTC
AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCCTACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAA
GCGATGCAAAATTGTTTCAGAACCTTTGAGGTATGCACCTTGCTGAAACACCAAAATGGTTATA
CATTAAGCTTGTCTAAGCGGATTCCATATGAACCTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAAGAAATTCGTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATCTCTCTAGACCAAGTGTGTTGAAGATGTTTTTGTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCAGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCCTAACCAGAAAGACCAAAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAGAATCTTTGATAAATA
AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCAAATCATTGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTCTCTGTGTCTGGTAAATACAC
TAAAAAACACGCTTCACCCCTATTAGAAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKSDANCSE
PLRYALAEPTNGYTLSLSKRIPYELFSKYVNEKLGELENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKDKIKFEFSLD
QVFEDVVFVIGCGVENIDGDSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESHD
DVMNSESLEKEEAKEKEPLTKEDQIKKWIIEERLMQEESRKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQOKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDVFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGNSIIIEEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCACTCACAAACGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCCTT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACGTCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAATG
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAAACAAAGTTTACTGAAATGAAGTTAGATTACAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
GCGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTCTCA
ATCATGTAAGGGAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAADVPTAYMRRGYTVPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMDDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NNEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTGTGAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTTCTCTCTGAAATTTAA

TGCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTATTCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTGTATTGTTCTTCCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACCTATTCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAACCTCATTCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTCACCGCATTTGGGCGGAACGTTTCGACCACA
TTTCAGTAGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCATTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQLDLSALGKM
YSITRDVLLGYGMINSGINIIIFNNIHVESNLQWKVLLPQESTFETWKLELGQGQYHSI
EHYALHDNIMEEIEGPKDANKFHVLTALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVSR
ETVSGAETVNKTRIEKMSPLAVHVNVNLGGREEDGWSEKLSSTEIRLLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAAGCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTCTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTCTATAATGAATAGGTTTCGGGTAACGGTTCCCTTTTTTAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAC
AAAAGTGAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCCTTTTGAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTCTGTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCGTTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTTAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTTCGTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCCTAAGAACTTTAGTGTATTGGTGGGTTGTTAA
TTGCATTTCAGCGATTCAATTGTTCAAAAACAAGACAACATTCGGTATGCTTCCTGAATPAA
ACAGCAAAAACGACAAAAGCGAAGGGTTACCTGTTGTTTGTCTGGTAGAATTTAATTGTTT
TAATGTTTATCGCTTTCACTTTTCAGTAAATCATAGGTTTACTGTTGTTTTGACCATATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAACCTACTGGTTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNATGVLCAVISQALVYGLFTGSSFVLRNFSVIGGLLIASFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNLIIIGLLLVNTGAGE

ATTCATATTCATTGAGCTATACGAGGCAGTGGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAAGCATCAATAGCCACCAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAAAAATTCGTGGGCCTATGATAATTTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAAACTTTAAGAAGGGTTCACATTTACTAACTATTTCTTTTCTTCTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTCCGTTACGCCGGTAAGAAGGTTGTTATCGTTA
AACACATGATGAAGGTTCCAAGTCTCACCATTGGTTCACGCTTTGGTTGCCGTTATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTCATCAAGGTCGTCAACTACAACCATTATTGCCAACCAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA
ACCAATGGTTCCTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGLVAGIERYPLKVTKKHGAK
KVAKRTKIKPFIKVVNYNHLLPTRYTLDEAFKSVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTACCCATGCACCATTTGGATTATAAAGAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTGAGAAGAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAACTTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCACCAGGACGTGGTGGGAAATGCAG
CAATTCCTCTCTGCTTCCCGCTGACCTTTCTTGGGCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAATATTTGAGGAATGAATTCGGATGAAATTTCTAGTAGAAGAAAAAG
CCTAAAATAAAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG
ACGTGCAAAAGAAAGCAATTAATTTTTAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGAATGCTGGGTAATGAT
TTATCCTTCTTTTTTGGAGCACAAATGCTGAAAGATTTTCTCTGCTCTCTCTAATCTTCTG
ATGTATCCTACCCAACCCTACAGTTTTCAAATTACTAACATCAATTTTTTTGTGAAACGA
CTTTCGTTTTCTGTTTCTATTTATTTTATTACAGTTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGGATGTCAAATGCCCAGGTGTTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAAGTGTGCTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVFSHAQTAVTCESCS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTGCTACATATTTTTCATAGCATTCTCTGTACAAACTTCAAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTCAAGCGGAGAGACGACCTCTAGAGAGACGTCCGTCGGTGCGGCAAC
GCTGACGGTTTAGTTGTTTCGACGGGATGATGGGTTCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTATTCGTGAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTGAAGGAGATTAAG
CAAAAAACAAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGGAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCATTTACAGAAA
AAAGATACAAC TAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCTGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCVRKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGACAGTATCTTAATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCTGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAGACCAATATAATAAAAAGTTATAAATTAACATTTCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCCACACCCACACCCACACCCACACACACACCCCA
CACACACACCCACACACACCCACACCCACACCCACACCCACACACACACACACACCCCA
CACACACACCCACACCCACACCCACACCCACACCCACACCCACACACACACCCATCTA
ACCTGTCTCTTAACCTACCTTCACATTACCTACCTCCCCACTCGTTACCCTGCCCCACT
CAACCATACCACTCCCAACCACCATCCATCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAATCCACTACCATTACCCTGCTATTAC
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPHPTPTHHPHTPTPTPHPHPHPTPHPTTPTP
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTITL LLLPYHPPCPTHCTVVLP SILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAAGTTATAGAAAAGTACCGTGAGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTTGAGGGGCACGATGCTCTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTTCTTGTAAGGATTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTTCCGGGTAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAAATTG
CTGTAGAGATTCTGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTCTTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTGTCATCATCATCAT
CACCAAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTC
GAGCGATGTTGAAAGAACC AAAAAGGAAAAC TGTGATGATTTTCATAGAAGAAGAGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC
CAGAAAATGTGGAAGAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCACGGCACCCAACCTACCAATAAACTTGGTCGTCGCAAACTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACAACCTTTCAAATATGAATCTTTCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAAGTGTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCCGATTTCCCGTAAATCAAACCTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAAGTGTAAACTGCTAT
TAGAGGCAAGTGCAGATCCAACAAAAGAGATAAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAAACAGTGAAGAAATTC AATTGATTGAAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTA AAAACAAATGCCTTGCAAGATGAAGAAAAAATTA AAAAGTATCTCACCACCTCTA
TGGAACCTCATTTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAAGTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
ACAAAGAGATTTTTGCGCTATATTTTGTAGACGAAAAAAACGATAAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
CTTCTGAGAAGATTTCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT
ATGTTGTAAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CAGCATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKEPKRKTVDDFIEEEGLGAVEEE
DLSDEVLEKNTTEPENVEKDIEYSDSDKDTDDVGSDDPTAPNSPIKLGRRKLVRGDLDA
TTSSMFNNESEDSELSDIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSDNSNKS SHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTP LIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKRLSIAAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGRLPYVGTYVENGKIDLRSFESVTKCGHEDITSIFLAFGFPVNQTSRDNKT SALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRKTALYYAKNSIMGITNSEEIQLIENAIMNYLKK
HSEDNND DDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKES'TTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPLSMEPHSPK
KAKSVEISKIHEETAEREARLKEEEEYRKKRLEKKRKKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRRAVRDLYPLGLKIINFNDKLDYKRFLPL
YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDP SHLTPLWNMLKFIFLYGG
SYDDKKNMNMENKRYVVNFDGVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQRLKIPREL PVKFQHRMSISSVLQQTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAAC TGAACAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTGAACATCGGCGTTTAGGCTTGTGTGTTCTGTACACATACGCTGCTTAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTTCAATAACGATTTTGC
GAAGGTTTAATTTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATAT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTTAAGTTTTTAGGTCAAAAACAAATTTCTACCTTCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTTCGTTGCTG
CCTCTGTTAGTAAAGCGGTGGTTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTGTTAGTTCGTTAAGTTCAAGTGGGAGAAAGAAATCCAGATGTAATATTTGTGTGCT
TTCATGGTGATCAGGTTTTGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG
AATTGAGTGAATTTCAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCAATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTTCGGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAATGTACATTATAAGCACATAG
ACGGCAGCGCCTCATTTCAAGAACTTTTGATATTACACCTCCATTTCGGGCAAATAGTAA
GGTCCCATATATGTACAAAGTTACCTTGTCTGGTTTAATTGAACCTGATGCAAACGTAA
ATGTGCTAGCATCATCATGTTCAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG
AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT
CCGGTTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAAGCGGCCATTATAGCATAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAAATTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACGATCCTGCTTCTGCTAAGCCAGTATTTCGGCAAACCCGCGTTTCGGAGCTATTG
CCAAAGAACCGTCAACATCAGAATATGCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTTCGGAA
CTGCATCAAGTAACGAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTTCAT
CATCTTTTGCACCCGCCAACAATGAACTTTTCGGATCAAACCTTACTATTTCAAACCTA
CAGTTGACAGCCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAAGACCAATGCCTTTGATTTTGGGAGTTCTTCTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTCACCTTTCTCTTACAGTTAGGAAACAAATCACCATTTCAGTTCCCTTCACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATTTCTACTAGATTACCGGAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG
AGGAAGCGCAAAAATCCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAATCCGAAT
CGCCGTTTTTCAGCATTGTGAACAAATATTACCAAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTACCAATGGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAAGTGCTTTTG
ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCAGGATAACAAGTCTAAAGAAA
TGAATGAAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCGAAGGAG
ATGGAATAGCATTGAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACAAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTCTGTTCAAACAT
TTGAAGGTGACGAAAATTTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAAGATATT
ACACAAGTGCAAAGTATCAAATATTCCTTTCTGTTTCAAAAATTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAATATTCAGA
ATAATATCAAGTGTGAACAAATGCAAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGTTATGTACAGGAAAGATATTGACAAATAACTGAAGATGTAGCCAAATGCAA
AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAGACATTACGTCAAAGCTATTTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDVFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQKKNVNNLTVILNSVNDLSALDLRTKSTKQLAQNVTSFQVNTNSQLAVLLKD
RSFQSFARWNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPFPQGQIVRFPYMYKVTL SGLIEPDANVNLASSC
SSEVSIWDSKQVIEPSQDSERAVLP ISEETDKDNTNPIGVAVDVVTSGTILEPCSGVDTIE
RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTSEKIPIAGQEQUEEK
KKNNESSKALSENPFTSANTSGFTFLKTQPAANSLSQSSSTFGAPSFSGSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFSGSKSS
VESPASGSAFGKPSFGTSPSGSGNSSVEPPASGSAGFKPSFGTSPSGSGNSSAEPASGS
AFGKPSFGTSAFGTASSNETNSGSIFGKAAGSSSFAPANNELFGSNFTISKPTVDSPKE
VDSTSPFPSSGSDQSEDESKSDVDSSSTPFGTKPNTSTKPKTNADFSGSSFGSGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHNDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK
LEDINTDELPHGGEAFKAREVSAADFDVQTSLEDNYAESGIQTDLSSESKENEVQTDI
PVKHNSTQTVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTRLRIESTFQTVAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPAEIILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFL
MHFDDASSGYVKDLSTHQFRMQKTLRQKLPDVS AKINHTEELNLILKLFTVKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRLQLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKNL NMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTTCATTAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTTCGATATTTTCGTGGAGCAAAACAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAAGGTAGTTGAATCTCTATTTGTGTGTATTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTTT
TCGAACGTTTCAGAGCTTAAAGGGACAATTATTTTAGAAACTGAATTTTTACCCAGTGGAA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACCTTTCCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAAAATATGATTAGATTTTGTAGCGGGTGATGCGACTTAACAGTCTCATTGCCCT
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC
TTACTAACTTGTCTATTTTTTTATAAAATTTATTTTTTTAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAACAATGTAATTATATAAATATGAAACAT
CTCATATTTTTAAATGTCATAATGTCTATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTTAAGTATGAACAAATTTTGGGTTTATTTTGCCATTTTTTTTACGCGG
GTTTCTTGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAAGTTGAATTTATGG
AACGAAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTCAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACACATACTTTTA
TGGAGAAATTTCAAACGCAAAGAAGAACGAAGATAAACAAATTGCCAAGTTTGAAGCA
TGATGAATGCAAGAGTACATACGTTTCAAGTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAAAACGGGCTTTGCATGAGATCAAAATCCTTTCGGTTGGGCAAACCTTTTTGCTAAAA
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTCTCA
CCATAACGGGTTTTCAGCATAACATAGATGTTTATATCTTTCGGGAAAAAGGGGTAGAAA
GATATTATAATCTTCGCCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTTTCATAAGTGTGCGATT
ACCATAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTAATGGTGGGT
ACGCCCTTGGGCGCGCTACGAAAGTGGAAGTCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAAATATAATCAAAGGTACTCGTAAGCGCCTGTGAGAAGAGGAGGAAAGAC
TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCTGCCAAAGCATTTTTCGACGAGA
AATTTCAGAATCCAGATATGCTGGCAAACCTTAGACAATAAAAGAAGGAAAAATAGAAA
CTAAGAAATCGACAGCACTGAGCCGCAACTAGGCAAAATTATGAGAAGGAGGGAATCCA

GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTCGATCCCACTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGAT
CCAAGGAAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTFEGSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFSLWVKKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQEPYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKCI LEI
GSSRDVLGWCPIVNNKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
KVD SQPSLYKAKGENGFNIIKGRKRLSEEEERLKKSSHNTNSNSAKAFFDEKFNPD
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDLLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETS DGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGA AAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTGCTCAATTTTGAACAATGGTAAGACAA
ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACTACAAAACCTAGAAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACCTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTCGAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCGGTCTGCTGTAGAAACTGCCGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTGTGAGATATGCCGATGACTACAAATTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHSGSKTLYVHPFDNETIWEHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVAVETAGCDVLNLSLKKGSPVTLKLT SVATSLASPYIASFA
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTTCGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAATATGCTGCATAGTGT
GAGTCCCTCTAGTTTTTACCGCAGCCACGCGCTTCTCGAGCAAAGTGATATCCATT
AGGACTCATCATTCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAAATAGAACC
TTCTGGAATTTTACCCGGCGCGGCACCCGAGGAAGTGGACAGCGTGTGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAACGTGTTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTTGCTGTACGCCCTTTTCGTGGTAATATTACCTTTACAGAAATCTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGTGATGTAGAAAACTACGGAACCTGTTATCG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTCACCGATGATG

AAAGATTGATTGGTGTATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTTCAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCCGCTGTAGAAAGTAAGTGTC
AAGGAGAAAAAAGAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTTCGTTACTGTTCCCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCTTGCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAATTATTGTTTATGATTTGGGTGGTGGTACTTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGTACTATAAGATCGTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAACCTTGACCAGAGCTAAGTTTGAAGGAATTAACCTAGATC
TATTCAAGAAGACCTTGAAGCCTGTGCAAGAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTGGTTGGTGGTCTACTAGAATTCCAAAGGTCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTGCAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAAATTAAGAGAAATACTGCTATTCTTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTTGAAGTCAACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAAGTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACCTACGCTCACTCTTTGAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTTGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTTCAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTTGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLRGADDVENYGTVIGIDLGT
YSCVAVMKNKTEILANEQGNRITPSYVAFDDERLIGDAAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAAVTVPAYFNDAQRQATKDAGTLAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVFVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKT
PVEKVLQDSGLEKKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGAAV
QAGVLSGEEGVEDIVLLDVNALTGLIETTTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRILTQEEIDRMVEEAKEKFASIDASIKAKVESRNKLENYAHSKLNQVNGDL
GEKLEEDKEFTLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDGDFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTAGTTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTGACACGCTGTCCAGTTCCCTCGGGTGCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAATAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCCATATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACCTAGAGGACTCACACTATGCAGCATATTAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACTGGAGTAGCAC
ATGCTGAGTTTCATGGGGATCGATCAGATCAAGCGATGTTGGGCTCCCGAGGAGTTGTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTTGGTGTTCGTTGTGGCAACGAGAGATTGGAG

GCAACGGTACTGTCTTGTCTAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGT'TTTCGGAATAAAGTTGACTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCACCAAGATAATATAATCCAAGAACTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFSGCNERFNGNGTVLS
VNHDTCTLVPKNNSAAGYESIPGILRKEATMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTECFANKVDLSSNSVDWDLIDSHQDNIIQELLEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCTTCTTGTAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCCCTTTGGGT
AAAGTTACCAGTGTTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAATTCGGAAGAA
ACTTGAATTTGAATATGATTCTGCCACTTTTCTTGTCTGTCATTTATAGTCAGAAATG
AAAAATTGTCCGAGAAATTAAATATAATATATGGAAGAAAAAGGGGACATTGAGTTTAAAG
AATTTGATTAAATGTCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCCATCTGTTTGAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAACAAATTTGATCCACTTCTTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAAATGAAAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTGGTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAAATCTGGTTTTGAAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT
TCGATTGAGGATTACAAAAACAATACATTTACCATTTAAGTAATCAGGAAAAATACGC
AAAACCCACTTTTACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAAATTCACGAGGTTTACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAAATGTTCCCTACAGAG
ATTTTTATAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCCTGAAAGGATAGTTTATC
AAGACCCGGAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTGATTGATGATGAATCTTTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAATCCTAACAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTCTTGGAGTTTGATAATTTTATTG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTTGCCAGGATTTTCCCAAATATTCAAGGAAATGTCGTTCAAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA
TAGATTTCATCTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAGTGTTCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAAGTTAATTTTCTGCGGTACAAAAATCTTCAAAATA
CAATCACCCTAAGAAATTTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGCTATACAGGTAGAACCCTTTGGGATAGTGAACAATGATTCAATATTTATTTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCACTTACTGAATTCGCAAA

AATCGACCTTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTACAATAGTTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGTCTGAACCCAACAGATTTGTGCGAGTTGTCTGAGAACAAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACAAACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCGGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSSENDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYGNESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNKNDEKWFLYPKPLPKFWRFEDDKRFQDPDS
DLNDDGDSTGTGAATPHRHGYYPFYFTDHYYYTKSGLKGKGNIKVPYTGIFYDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLNSKKEILANKNPYRDFYNSRKVDRDLSLSCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSINFQEFDLI
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPVTAHYMYIYKSLAKVNFRLSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDTATMIQYLFYLFQIPILAAPLSSVSLNSQKSTFLKN
KNVLLEHDYLDQETAKINPSRDI TVGEQRSYETNPFMKFMKGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGVKKAPYFEENVG
GIDNWDYDTAKDTSIKHNVPMIRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTGCGTTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTGTTCGTCTTTCGTATATTGC
GGGTTCGCCGCGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGCAAGAA
TTCTCTAAAACATATTCTATACTTCAAAGTTTTTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAC
AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAAATATCAGTTCTGCTAGGATGCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTTCGGGTGTCTTAACGCATTCGGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCCTGGT
ACGGGGAGATAAGCAAGTATAATTATCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGAAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAAACTACCTGGGTGAGT
TTGCAGAGGAAGTGAACCACTTATAAGCACTGTTTCCTCGTCCTCATCCTCGTCCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCCGCTGTAG
CGCAAGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAATCGACGA
CCATAAACCTTGCCAAGACCGCTACCCCTCACTGCGTCCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGPTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCGTCTCTAGTGATGCTACTTCATCCACTACCACCA
CCTCATCGTTGCTACATCGTCCAGTACCCTTCTTCCGACCCTACCTCGAGCTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTCCAGCGCGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAAGTTA
ATTCTGTTAAGTTTGCAAACACAACCTGTGTTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG
CAACGAGACTTTGGGTCACTTCCAGAAGTTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTG
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATACCACAAAGGACACCGCCACCCTTCAAGTAACCGCCTCAGAAAGTA

TCAC TTCGGA AACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTACTCCAACAGTGCTTCTGTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCCACTTGGACCCTACCGACAACCTCAGTAGTCCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCCCTAGCTTCGCCATCTCCACTGCCACCACCCTG
AAAGCAATCTGATCACAAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA
GCAC TTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACACATCGCCTATGAAAACCA
ACACGGTGGTTCAGCTTCTTCTTCCCTTCAACTACAACCCTTGTCTAGAAAATGATG
ACACTGCCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG
AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTGGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTTCCCTCGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTCCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGLVAVKAQTTFPNFESDVLNEHNKFRALHVD TAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTD TGAVDAWYGEISKYNYSNPGFSESTGHFTQV VWK
STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSSTESVGS
STVSSASSSSVTTSYATSSSTVVSSDATSSSTTTSSVATSSSTSSDPTSSNTAAASSSDP
ASSSAAASSSASTENAASSSSAISSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTSSVSASLSSSVAAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVS VTSVSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSPATNCSSIV
KTTTLENSSTTTITAITKSTTTLAT TANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTQLVSTCTSESDYSDSPFAISTATTTESNLITN
TITASCTTDSNFPTSAASSTDETAFTRTISTSCSTLNGASTQTSELTTSPMKTNTVVPAS
FFPSTTTTCLENDDTAFSSITYEVNAATIINPGETSSLASDFATSEKPNPTSVKSTSNE
GTSSTTTTYQQT VATLYAKPSSTSLGARTTTGSNGRSTTSQQDGSAMHQPTSSSIYTLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCATTTCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCTTTCTCAACATCCCTATTTAGTGACACCTTTTCCCAAAACTTCT
GTGAAGTTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTCCGTATTCTCTTTGTAGGGTTTCG
TTTGCCCTTCAAGTGTTTTGTTCTTATTTAGCCTTTTCCTTTACCTTAATTTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATAAAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC
ATAATACATACTTACAAACATGTACAGATAGCACAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCATATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAGAACTATTTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTTGGATTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTGGCGTTCTTA
AGCTCACTGTCAATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTTT
TTCACCTGTTACTTTTTTAATTGCTATATCTTTAAACTCATTTCATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAAGTCTC
TCTTAGCATACCTATTA AAACTGGAGTGGTTCGTCCTATCCAGTCTTTCCATCAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCTCAATTAGTTGCAAGATTGGAGGCAACAGTGATGTTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAACTGTATTAACCACAAAGT
CTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAAAGATACTGCGAACTTAATTTCCCG
CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAAAAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGC FIVNSIRLKLPRFYS LNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRTIKTP LGNGIIVDNAKSL LAYLLKLEWSSSLSLIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDV IKNQLLRYLDTDLLVFS PMNEFEGR LRNA
QNELYIPIIKGMEEFLRNFSSSNIRLQILDADIHGLRGNQQSDIVKNAAKKYMSSLS PW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCATTTAGTTTCAAACAAGATCCTTGTATTTATATAAAACAAAGATATA
ATTTTTTAAAAAAAATTAGAAAAAGCAAAATATAATTACAGGTCCCACTTGGAAATAATGGCA
CTGTATTGATGCATTTTCCTTATGCTTAGTGACGCGT'TTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCCTCCAG
GACAGTACGCGCAAACTATTATGGAGATATTCAAGGAAGAAGAAGAAGACTTTTTCGG
CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTACAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATTCTTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCACATTTGATCGCAC
GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAATTTGCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCAC'TTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCTTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCCGAGTATCT
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTAATGTTTCCATTGTTGAGGA
CTGGAGATT'TTGAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCTGGGTAATGCGAGTGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAATGACAGTTCATTTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTTTAACAACCAGTCACTCATTTATTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAAATACGATAATATCTTTGGAAAAATACCCAAGTAA
GTGGTGGTCAAATTACTCATGGCAAAAAATTTACCGCATCAATTACAGGTCTCTATTA
TCCAACCTGCGCATGGGAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTCAGTTTCATCAGCAA
TGGATCTCAAGCATTCAATACAGAAATGTTCTCTACAATAATGCCCCAAGAGTTGACGC
AGGACGTCATCGTTCAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDPVPRHLHKSCTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQITLSESI SLMFDRTVSIFRKCTIEGGFPHLIARLYRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNIIIEIFHLLDGLAFFKVNPDLSISTASAETIFRSISEGNHGV
LELGRSLMFLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANFNEDNNGLLIVDRNIPTDDFTLASTNRQSPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVVITDENTIISLENTQVSRWSNYSWQKISPHQLQVSIQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTTEAVSHSNQDATASPLSSVSSAMDLKHSLLQKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTTTTTATTCCTC
CGGGTGATAACGACGCGAAAAATATTTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA
CGCGACGCGAAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA
TGTATGCGTGTGTAACTATCCTGCACATCATCTTGCAGTGTAGTCCAATAAAAAAGGA
TTACTACTGTAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGCGGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA
CAGCTTTGTGACAGGCTAACTCCAAATTTCTTGGGAAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTTAAAGGTGGTCTCCGTTC
ATGAAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCTCATCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATACCCTGCGAAATGAGGATAC
CAGAAACACCAGTGAAAAAATCACCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCTTTAAATTTTGTGAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCATAG
ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAACAGTTTACAACAATTCAAAGATGATTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCAACTAGAAAGAACC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGCTACTCTCCTCTGCCATCGTGACAAACACAAGTGCAGAGACGCATTCATATCTT
CCACCGATTCTTCGCCGTAAATTTCAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCCACGGTCTACCAGGTTACGTTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCCCTTGAAACGCATATTACTGGAAATTAATACTAA
ACGAGGTAACAAACCAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCCTGGAAGTTTCAAATTCATACTATATTATGACAGAATTGTGCGAAAAATGGTA
ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAAAAATCATCGTGGAATTAAGCCTGGCTTTACGATTCATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTTGAAAAATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTCAATAACAATAGTAATATCAACAACCTAATATGAATAATGGCAACGATAATAATA
ATGTCAAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTTCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPYSNNKL
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQWFPKNDARTENTSSSSSYSVAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPEPVPKKSPLVEGRDHKHVHLSSSKNASSSLSVSPLNFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHNRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNVILKNRELNTSLQQFKDDLYGTDENFPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLLISSNKL SANPD SHLFEKFTNVHSIGKQGQFSTVYQVTF AQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGLDGFLO
EQVIAKKKRLLEDWRIWKIIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLPDNGNAWH
KLRSGLSDAGRLSSTDIHSESLFSDITKVDITNDLFDFERDNI SGNSNNAGTSTVHNNSN
INNPNMNNNGNDNNNVNTAATKNRLILHKSSKI PAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCTCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTTATATGATAAATGGAACAAAAACCTTGTTTTATTTACA
TACTTTTTTCCACACGTGCTTATGGGCCGATTGTATAAATAATCCAATAACGAAAAAG
AGTGAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTCAATCTTGGTTCTTCTCCAGTTTCTTCTTCTTAGCGTTGTAACGGATAGTGTTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAAAGGGAACATATCGTGCACATACGA
AGTGTAATTTGTAATAAATGTTAGTAACAATGTTCAAATCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSSQSDPLWQWSVLLLSLSHFLDSERL
LSLIKRETYRAHTKCTIVKNVSNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTCAAAAACTTATGGGCGTTTATAGGCTCCGGCTCAAACACCACCACGCG
GCAGGCCGAGGCAAACAGTACGCCCTTGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCCTTGCGTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTGCGAGAACCGAGAATTATTCTTCGCCCTTGATAGATACTTTAAAACTTCTACTTAAT
ATACTTTCTACAATTTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACCTGATCAATAGCAAATATAAACACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAATATAGGGAAAGGATTAGGAGTGTTAAC
CATACTAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GGTATTGCCCTTGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTAATTAGGCTCAAAA
GTCTTTACAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCAATTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCACGCGCGAGCGTAAACGCAAGG
ACCATTTGAGCTTGGAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAGGCGTACTGTTTGC
CTCGGCTTCCGCGTGGTGGTGGTAGTTTGGAGCCGAGCCTAAAACGCCCATAGTTTTT
TGAAAATCAAGCTAAAAAATGAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATT
AATCTTAAATTGTAAGGTTTTTTAATGGCCTTTCAGTTCTAGTATTTTTATAAAAACA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCATTTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT
TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFYIDHRSGK
IVVQLNGLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTTSAGIMDHEEARRH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTCATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTGAAAAAAGGTACGCTTCCCTGTAT
AATCAGGTATATTTCTGTTATTCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCCTT
GAAATTTGGTTCGGTTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAAAAATAAAGGGAGGAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTGCAAAATGGGTTCCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG
TTTATAATGAAGATCCCGATTTACCCGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACCTAATCTTGGAACTAATGGTCAAG
ATGGAAGAATGTCTTAGAACAACAAAGAGACGTGGTTGCTAGACTAATAGAAGAAAAACA
AGGAAACGCAAAAAAGGGGTGATAAAGTCTGTATTGTCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAT
GGT'TTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCCGTGGATT
TTAAAAATTTGGTTTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAAT'TCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAACCCGTTTACAGCAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATTTTGGCTT
ATAATAAACTCGAACCCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAAT'TCTGCGTTGCAATGCCTGGTACACATTCGCGCAGTTGCGTGATTATTTCCCTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTATAGCCTTCTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGTTGATACAGTGTGGGATAAACTATAAAAATTTTCCCATGAACCTCTC
CACCACCTTCTTCTTGAAGTTGAGTTAAGCAATTCGTCCTTATATGGACTTGAAGAATT
ATGTTGGTAAATGTGCGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTAACTTGCAGG
AATTGATCAAACCTGCTGATGACGTTATTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCTTGAAC
CTGTAGGAAATCGAACCGATTTTGTCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGCTCTATTAAGGTGAGCGCA
AGGATAAATCCCTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA
CTGTAACAAATAATGAAAATGTAATAATACTAATGATCGGGATGAAGATATGGAATAA
CAGATGATTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGCGGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGGCATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTGACGATTGTCTCCAATTATTTCCAAC
CAGAAATACTAGGATTAAACCGATTTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAAACAAATACAACCTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC
TGTATGCAGTAGATAAACCCTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA
AGAATTTTGCCGACAATAAATGGTACTATTTTGTATGATTCTCGAGTAAGTGAAGTGC
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCCCGCTCATAAAGATG
GCAATGGATTAGGCAGCTCTAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATGATGATAGATGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGCTCTGAAATATCTGAGGGAT
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVLDLMNVLDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFN

LSEIYGMTSGSPVVTNLVINQTTGELETEYNKWFFRLHYLTKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFFEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPPIKLLIPDMFENRLDKITSNPDLVIEIKPIEGNHHWPSNYFAYNKLLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLLDLSLHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKLADDTWEMHLKRNCSVITDLFVGMKYSTLYCPECQ
NVSITFPDYNVDTLPLPVDTVWDKTIKIFPMNSPPLLELEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQLLIKPADDDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFGVPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTFISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGLVMQVDDDEGDTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF
SDKIDATVNFPIITDLDLRYVVKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK
WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSSKLQEIIOKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMI ECNEDVQAPEYSNRSLEVGHITQDCNDEDDNDGGE
RTNSGRRLRLLLKKVYKNNSSGLSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCATAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCC
TAAAGCGGGCGCTCACAATATCGCCGAGCTACAGCCGTTTTTTTTTTTTTGTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTTCATCGATATAAA
GAACACTGTTTCACTTCGATGTATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTACACTTCTTGAAGTACAATGCTGCCAG
AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAACCTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCACTG
CTCAGACGGTCGCTGCCAAACCTTCTCCTTTTCAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGGTCGTCTTCCGCATCGTCCGTCTCTCCACGGCCAACGAAAAATCTGCAATTAG
ACACTTAGTATACGTTTGTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACCTGATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCAGGCAGAAACGATCGAATTGCTAAATTCCAAAATTTCCCGAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTAATTTTACCAAGAAAG
CATACAAGATTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGCGAGTGTGTCGCCTTTTTGTGGCTA
GTGAGGCCATCCCATACACATTACAGCATTCCCTTGTACCCTACTTGTAGTCCTTTTCA
AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCTATCAATGTGGA
TTTCCAAGTTCGACGACCTGTTCTAACATATTCGTTGTTATCTCCCTATTGGATGCCA
TGGATCAGATAGCCCATTTGCGCAAGCATTTGGTGTAGGTGTAGCGTTGGCTGCAATA
TCGGTGGTATGTCTTACCAATCTCTTACCTCAAAACATCATTTCCATGTCTGACTTGA
AACCTATGGTATTGGCTGGGGCAATCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA
CTGTGGCCACTATTTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT
CAGGTCAAATTGCAATCATTCCTCATCGTTTGTGTGTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTGTGTGTCATTCTATGTATTTTTCGGTATCCTGATGTTGGTTGTGG
GTACTTTTCGTCTCGCATAACAGTATCCGCTATTATCATCATTCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTGTTCGGTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTGATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTCTATGTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAPPEWQNHMYDYSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRMKEKIFYKRRSSSA
SSVSSTANENLQLDITYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPPDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLCLQKSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRMALVECVAFWASEAIPHLITAFVLVPLLVLFKVLKTS
GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIIITVTATILLWCVESQIEGAFSSGQIAIPIVLFFFTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSHT
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVT AISKVDKGR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTGCTTAAGTTCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATCTTGTGCTTTTTTGTMTTATCTCTTTACTTA
CTTGTGCGCTTCCATTGCTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCCTGGGCC
TCTGTTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGTGCTCTTTGAAATC
TGACCAGAACTGAGTTGGCCTTATCTACATTTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGGCCTTGGCATATAACGGTGTGTCACTTTTATTGTCTCTTTTCATG
CATCCTGAAATTATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAATAACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAATGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT
CTCTCGTGAACGGCAATGCAAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTTCACTATGCCTCCACGGCGTATGGTGTAAGAATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTTGTAAGTTCCATTTTTTCAGAGACATGTACCACCCGTTATGTCGTTTT
CATTAGGGTCTCTAGGATTTTTAACAATTTTAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAGTGAAAGTCTCGATGAAGTCAAGGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAATAAAGTGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAACTGCGAAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCCAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNINGVDKWVNEEDGRNDHHNNNNNLMKKAMMNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANS GGGS INGT RGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHDVFFDLVVTLG DGT VLFVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRRLRLECTIYRRHRPEVDPNTGKKICVVEKLSHHI
LNEVTIDRGPSFPLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGDRIELQKGFITICASP
YAFPTVEAS PDEFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDES VNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTCGAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCAATTTGTGTTCTATATGTGGATGAGGATAGCCGCTTTCTTCT
CATCGGAGGCCATATCATCTTTGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTCTGAACTTTTTTTTTT
TTTTCATGTTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTTC
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGAAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTGCGCATATGTGCTG
AAGGGTTTGTGTTGTTCCATCTTATTTGCATAACATAGTTATATTTACTTGGTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACCTTATTTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAAGCTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACGTG
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTLS DYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCGTGGTCTCCATATCTTTAA
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCAATCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGCGTATTGTTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTTAAAAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTGCTGCCAAAACCTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCCTCATGGAGT

TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATT
TAACCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTCCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCCA
TGGCGTTGTTCGGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT
AFPOQTSYMMQNHLTLQPVADYHHMVDLASTADLQSDIAQSFPTQFQTFITAFPWYT
SLLNKASATTIYLPQHFIETGETEATMTNSSYASQKNSVSNVFPSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCCTTTTTCTTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA
CGGTCACCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGGGTAGG
GAACATCACCTTCTCTAGTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCGCA
TTTAATCATATTTGGAGGTCAGAGGACCAAAAGGTAATTTAGAGGAATTTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTATTTGGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTTTTTAGGTCCACCAAGA
ACCATACGTTTCAATGCTAGACCAGATGGTGTTACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG
GTACTTGTGGCTAGAGAAGTTTGTAGACTAAGAGGTGCTTTGGTCGACAGAACTCAACC
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDRPLDAQAIKEASYVNIPIVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTQPWSIMPDLFYRNPEEVEQVAEEAAAAEEGEEVEEVEGQAEAT
EWAEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGTCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAATACATACATTT
CTGAGAATGCATTGATGCCTTCAACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGTGCTTGGCGTTCCATGGTTTAATTCAGATGATGAATTCATATTTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAATAATAT
TATGCCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCTTCTTTATTTGTTATTAGCACACGTCAGTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTGCCATAAGTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCTTGGTGATATCATTTGTTGTTTACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCCTATCATACAGGTTGAAAAATGTTGCTT
TTTTATATTTTCAAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCTAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAC
TAAAAAATTTAGTACTATTAATTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTGTATGATGAATTTTCATGGATTTGATATAATAAACAACCTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTCGAAAGAAAAGCAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIIVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVLDYSSTEDEFYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHGLPSDQLTNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPeamFRSINNLEKFHQSSFFYL LLA PRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFLVSTSLLMINFAMALLIGTLAF
PMTFVKTI VESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVL
LILTNPFISITLFGFLFFDDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTATATTAATAAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTCGTCACACAGTC
ACTAGTCACTTGGTCGCATTCAATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCCAAGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTCTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTTGTAACAACGCCAAGCCGATAGGTGAGACAATTCTTGAAGTAATGAACTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAA
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCCCTCCGTTTCGCAACCGTGCTCTCTGTTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)
MKFQYALAKEQLGSNSRSGVKLISKHHWLPEYYFSDLFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMVGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)
ATCAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAAATAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGLATCT
ACCTGGGGTTAATGAACGAGAAAGTTCCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACATCAAAATGAAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTTCGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGCTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTACTACAAGGTCGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTTGTGGTGGTGGTGTCTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGCTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)
MQIFVKLTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQESTLHLVLRLRGGGKKRKKKVYTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)
AGCCACCAATTCCACCAGGCCCCGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTTGCACTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCACTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTCTCCATAATTACCAGTTTGTCTTCTTTTCCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)
MGASSGRIGKSMLTQGTFFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)
GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTTAGCAAACCTTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCCGATG
AAAATGCATATATCACGTTTCTAGATGCTTCCCTGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAACAAGAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCCGTGATACCATTTGGTTCTGAAACTTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCCGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGCTAACA
AACCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCCTCACCT
ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGCTCAAAT
GTGCGTTAAACAATTTGAAAGATTTTCAATTTTGACTCCTGATTTTCCGGAAGAAGACGTC
TGATGAAAAAATTGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTTCTTTG
AAGGTCAAATTTGTTTGAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTTGTTGGTTATTGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTTACAGGTAATATTAATGTTTATACCTTGAAAACCTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAAGTAAGGAACAAAAGAACAACCTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCCCTCCTGGCAAAAAACATGGAAGACTTTGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTGCACCTTCATTTCGCCTTGTGCTGAACGACTTGATAAATAGTC
CACTGAATTTGTTTCAAGGAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTTTTCAGGGAATTTTCTTGCAATTAACCTTTGCACTAACAGATTTTAATGACG
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAATTGGATGCCCTACATTGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTCTGGCA
TGAAATTTTTAGAGAAAAATGACACCGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAATATTAATAAATAAACGCCAATAGCATTATCGGAAATTTCTCTCA
AAATAAATGTAAAAACACAACAGGAAAAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAAATGTCCGGAGAACAAAAAATTTGCTCCGCTCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLMOYTDGLSTHEKIIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPSVEGFESIRYLNIAASLYLPAVGD
TYFQRAKIYILITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGEKSFEGQIVLQFLSIVEHTLVPQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDFLMFTTRKSKEQKNLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRRKFCSTFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLTKVLPKE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTIITGPLSSDFLSYPDEAIDADEITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTCGTAATTGTTATTATGGTACATATTTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTATTATCC
ATTATCTATGGTGGCATGTGTCAATTAATGGAATATACTTTTTCCCTGATAAGTTTGCT

AAAAACGGTCGGATCATAACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA
ATGGCGTGAACGCGAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAACTGT
CAATAAAGAGGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCATGTGTGCGCAGAGAAAAATCTATAGCGA
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAACATATGATTTTCATGTTTAGTGGGTTCCCGTTTGCCAGAAATGGGGCTAACT
GCGAAGTTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT
CGCATGGGTGGGGAAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAATGTCAGCACGAAACCCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA
CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATTGACCAAGG
ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGCTACAT
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA
CGTTCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTACGAGA
CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCCAAACAATCACTAGACGACGAGAGAAAGCTATACCAAAGGGGTTCAT
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACC GCCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAAACACAAGTAACAATAACAAGTTCAAGTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAATGTTTTCGCCAGTGGAAAGAGAGTATACGAGTACGTGGCCAGGCACCTTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCCTTGTGTTGGACTGGGCGG
TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCCCTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCCCGATGGGAAACCAAGCAGTTTACC GCGGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCAAGCCGATGACTGAGA
GTGAACCTATTCTCCTCATGGATACAAACGGCATTTGGCACAGACGCCACCATTGCGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT
GCGAAGGTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAGCAATGCCTGCAAGAACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEKNIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPPFARNGANCEVTMTS
VAGHLTGIDFSDSHGWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD
CDREGEYIGWEIWQEA KRGNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHAVG
TRIEIDL RAGVTFTRLLTETLRNKL RNQATMTKDGAKHRGGNKND SQVVS YGTCQFPTLG
FVVD RFERIRNFVPEEFWYIQLVVENKDN GGT'TTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKS KPTTKYRPLPLTTVELQKN CARYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFPHAMDLKSLVEKQAQLDQLAAGGR TAWASYAASLLQ PENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACCEDAKGQSM TLVLWDWAVERFSAS
GLVV LERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAATAACAGCTCTTTCCTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTA AAAAAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAGAACAAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTCTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTATTGTTGTTATTCCGTAATCGTGGTGCTCAACTTTTGAAATTTCACTGTTTACC
ATAACGGAACATAATTA AAAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTCTAGTCCTCACATCACTAAATGGAACCTTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCAAGATGGTTTGAATTTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACACTTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAGGTATATATACGAGACTTAAAAATCCAGTAATGGTACGTTTATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAATATTTGTAC
AACCTTTATTAGAATCACCGATTTTGAATAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCTTGGGCTCTGATACAGAAATACTGAGTGAATTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAATAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAGAAGGAACTGTCGGGGAAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAGGGGAAATAGAAGACTTGA
AAACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAACCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAATATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVIPIPKPDGLKLRPVANSNSSSSSSSLRGK
RVDSHTFQSQRSDNGNFDNRVLSRNHALLSCDPLTGKVYIRDLKSSNGTFINGQRIGSND
VEIKVGDIVDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTTHLEYTNKLLVEKNQQLVQLQNGLRRLKLSGKYEKIIEQNRRNQVKQ
LERDHMFKKSFVKKRRNNEKQKSMEREIEDLKRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCAATTTTCAGAATCTAATCAATGATA
GTGTAATGCTTTGCTGCCTATCGTGATTGATCATTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCATTTTTTTTATTTAAAAATAAAAAATCACAGTTAATTTTTCATGATCTTGCAAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTGCTTTGCTTTTCGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTGTGATAAGATAC
GGGACGACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTTGAGTTTTTTCA
AAATGTGCATCAAAATACTTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAATAATGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAATGAGGAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCCGATAG
AGCTTCGTGATTTCGGAAGCCTTAAAGACCAGAAATTGAACAATTAAAAAATCGGCACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTTATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAAATGTTCCATCAAGCAATAATAATGACGAGGATACATACTATATTCTCAAATTT
CTCTTGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAATAATTTATTGATGCTGAAATTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTGTTTTAGTCATTCCTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCGATGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACCTTTGGAATCCCTATTTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTCACATTTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAATTTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTAAGTTGTTAT
TAGTTGGTAGTTTGATCGGCTTTCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAATTTTGGACTACAATTACCACAGCCAAATTC
TGATTTTGATTATAACGTTGATCTACAGTGAATGAGCAGCAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGCTATAAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCTTCTACAGGAAAAGTATGGCCATTAATTTTTAGAAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
TGTCATCTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTATATGATTTGAGAG
AGAACTATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTCCGCGAGTACGAAAGAG
ACAATTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCCTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTPDEHDFRKPATKVVTTQLTIAATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDNDDESSLIHLVKRIVEGSGDGNHSAPERTNV
YLWYVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLHFHCRKKILKNLELKYSECPRELRTROPYSENY
HLLGNEQSGAVTHGENVPSSNMNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDLTKVYSTTVFIGLSSFLVIPVSYLATLLNLKTLKFWPSVQQLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSTYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFLQLPQPILILIIITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTGTTTGCCAAAGATATGAAAAAGGGCACCAAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAAATTACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTGCAAG
ACTCTTTTACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTGT
TCTACTAAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTCGCACCAAAACCAGCTTATTCCACAAGCTTATATTT
CTAACTTTTACATAACAGATTGACAAACGAAGATGATGGTATCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAACTGAGTGTCTCATGAAAAATACTCCGCGACTTACAAATGGTGTACCATTGGACGGTT
CCGAATACAATGTCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAAT
ACGATGCGGGTTCAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

CTTTCATTAAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAAC TACAATGACGACTCCATATCTCCGGAGG
AATTTGCCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAA CTCAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTCATCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTGAGGACCATGTCC
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAATTGGTGGCCAAAGGGTGGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQNLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM
NGSNFNADTHYKDNVSHENTPALTNVGTMDGSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPNFNLRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSIISPEEFASIYC
KDLDMTSATLQTQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHPVNDAAFGL
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLKRETDRLSRRGRRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTGATGTCAGAGAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCCTCTCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTG
AGTCTATATGGAGACACCCTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCGTGCGCTTTGTTGCTCGGACCATGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTATTCCGAACCGTCCATGGTAACACCATT
GTAAGTGCCGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTTCATATTGAATTCATAAGAGATCGTTGTATATTCCGCATAG
TTGACCCTTTAGCCCTTTTATGCTGCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTGGTGCGACATTGTGTGCTGCTATGTGCCCTTTCTTCTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTTGTGCTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCLIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDITIFVCQ
SVMKVRNISLWNKLVLRHCVLLCAFLLSFFNVLSHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAAATAA CTGCTTCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCGCGTACTGGTGTCTTTTAGCTCATTCGGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAATAATGCCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAAAATTATGGAGAGTTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTATTTCAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAATGGCTAGAGAAATCACCGACATCAAACAATTTTGGAAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAACAAAAAATTGAACAAGG
CCGGTAAGCCATTGAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRTQTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTTCTTTTCTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTTC
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATGACGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAACCTATTTAGGTGATGTCTCATACTGCAACCACTGGAAAATGACGCAAAATATC
AAAAATAAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAGAGTGTGAATATGTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTGTAACCTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTTCGTGGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAAGTTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTTGTCTGCTGCTGGTCTGTTTGTCTTTCGTTTTTAAATTTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACCTCTAAAGTATTATTTTCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCCGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATT
ATTTACCTTTTCATCTTCAGTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT
GATTCAAAAGGCGAAGTGCGTAGGATTGTAACCTCCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACCTATTTTTCAATATTT
TCACATGTGTTTTCAATTTCTGCTTATTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTAAAGTGTCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCCTCAAAATCTCACTCTTAAATTTTCAATGGCAAAATCTTCCGCACAACCTT
AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACCTGAACGGTAGATTGAACCAATGTG
GTGTTATTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCAACT
TATTGCCAGCCAGACAATTCCGTTACGTTATTTTGAAGTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFEYIDHRSRK
IVVQLNGRLNKCGLVSPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAAATAAATATCATGTATC
TCACCCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAA
TACTATAAACGTTTTGTTTTGTTCTTACGCACAATATCCTTGCCTAGAAATCGTTTTGA
AATTTAAATTTTTATTACCATTTATTTGATTTCGCCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTTATTTGCGATAT
CAGAGTAACTTAACTAATATGCAGGGCACTTTTAAAAGGTTTTACCATCCCACGCTTA
CGCGGATGTCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA
CCAAATACTCCAGGGGAACCTTTTGAGGGATATGTTTGATTTCGGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAAATTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTTTCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTCAATGTTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGTCTTTTCTGGATACGTCTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGCAGGGAGGCTACTCCATCTGAAAAGGAAGCATTTGTGGA
AGTTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTGKGLFIAPVSYWKEDKALFFPHLI
GTAMDGKTKQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGIIVDDNKKTDYLTADARLS
LNDSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFECSRGQWPFVSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCCTTTCCCGCAACATATCC
CATACTCGAAAGTAACCTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG
GGCATTTGCCGCTACTAGTTTTCAAGGCATCATTAGTGTATGTCATGTCATTTTCATGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA
GAACTTTTTATCTGTGTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTTGAAATTTTGGATTTTTGTTATTGTTTTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAATAATTGCAAGATATCCC
TAACCTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
TTAAGCTTATTGAATGACAAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAAACA
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAGTTAACAAGAAGTGAATGATACCAAGT
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGTCAGAGCAGTTTAGCAGGGAACCTAACGGACCTTGAAAAAGATTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGTGGTACAAGGCGACGACAAAGAAGCTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTTCTTAACCTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAAACAACCTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACATATTTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACCTTATCTTCCTG
AGACAATCTGGCCCCGTAAAATTGACGATTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKEYWQYEITSKVQRDLGIVNELSISEKDDT
DPSKLGDIYISRDNVNLLNDKLEVPVIERQIENIKLQYENMVRKVNKELIDTLTDVDTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLTLLQDKKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPBKIDDFSSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAGAAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTTGAATTTTCATGTTTTTTTGAAAAATTGAAAAGGGC
TAAATTATCCGTCGGGGTGTCTCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCTTCCAGAGATTCGCC'TTTCAGAGGCAAAGAAGCTCGTCTCCGC
AGGCCTCTTGTTCGGGGAGGAGGAGAATTC'TTGC CGGAAACTGGTTGATGCCTGGGCTA
TGGTAATCTGACACCTTTGCTATCCTAAGTGGAAAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACATTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGTTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG
GATAATAGCTTAAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAACG
TCACGGGTTACCAAATACGAGGCCGAATTAACCTTACGCTACTATAAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGAAAATACAATATATGACTCAATGCGAATTTAAA
AATTTCACTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCTAGCAGTGGTGTGAAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC
CAATGTCGATGGTAACATTAAAATTGTTTACGCTTTGACCACTATTAAGGGTGTGTCG
TCGTTACTCCAACCTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAAATCATGCAAAACCCAACTCATTACAA
GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACCAACGTCGAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQQSFQHILRLNNTVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTYKI PAWFLNRQNDITDGKDYHTLANNVESKLRRDDLRLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTTCTTTTCTTCCTTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACTTAGTTAGTTGTATTTCGCCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG

CCCCATCCACTTTTGGAAAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTCTGAAGTTTGTGGCTGACTTGC
AAGGTTCTGAAGACCATTCTTTAGAAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTGGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAACCTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSSEHSEKVKLRVDEVQGNLLTNFHGMDFTTDLKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVLLKQPKFDVGALMALHGEESGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGCTTTTCCCAAAACAC
TACCTCTTGACACGACTTGTGTTTTCTGTTTTCTCTAAGAATATCACTATTTTCACTTT
TTTCACTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCTTAGCATG
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACACTACAAAAGAA
CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGACTTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTTCTTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAGATTTGC
AAAACCTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTCTAGAAAGCTTGGATTGGCTCAACCAACAAATATTAGACACATCGGGACAA
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTTGACCAAGACCCCAAGATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCCCTACAAATTTGTACTCCAAGTTTCAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTTGGTTTGTGACAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAAAATACCTTTTCAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCGGTGTTCGGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAACTGGTTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVSNPNFGWFGYTGSDDHPVSDWLFDTWSTD SLRNF

LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLWLNNDN
GIDYDKAVQSKDELVQKVKENIYRTSEKAEQRLGLLESLLDLAHQQIILDTSGQIKDITVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELKVKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFQVVPVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVKNWSKLSILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGATAGGAGAATTGATATATTTCACTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAAACAAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCTTTTGGTTTCTCTTATAGAAGACCCCTGGAAATTTTTCGCATTTTTC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAACTTGTTCATCATCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACTTAAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGTCATATACCA
CAGTAACGTGCAGGTAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG
CTTTTACACTGCAACTTCAAACAATAGCTACATCGCCACCGACCAAAACAAAAATGCCT
TTAATGACACTCACTTTTGTAAAGTTCGACAGGAATGATCAGTTAGTCCCAGTTGTAAACG
TAACATTCATGAATTAAATGCCATAAATGAAAACATTAGAGATGATCTTTTCGGCGTTAT
TAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACGTGTTTTACAATTGGCGAAA
CTGGTGAATCATTTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTTCCCTGATAGAGTGACAAACATGTATTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCACCATATTTACCAGAAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCAGCTGG
ACACAAAAATTTTAAACGAAGACTTAGTTTTCGCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCCGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAAT
ATGAGTTGATTGCACTATTACAGACTTTCCGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTGAAAAAATGTACGGGAAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGAGGCAAAATCGATTTCGTTACACCA
TAGAGAACATCAATTCCTACTAAAGAAGGAAAGAAAAGACTAACAATTCTCAATCACATG
TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGGAATACTGAAGTTAACAACGTTTGTAGAAGCATTGAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGGAAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTONAFNDTHFCKVDRNDHVSFSCNVTFNELN
AINENIRDDLALLKSDFFKYFRLDLYKQCSFWDANDGLCLNRACSVDDVVDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLI
LTANPERFTGYGGKQAGQIWSITQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNTKTGKWEPLDLFMARIGNFPDRVTNMYFNAYVAKALWKIQQPYLPEFSFCDLVNK
EIKNKMNDNISQLDTKIFNEDLVFANDLSLTLKDEFRRSRFKNVTKIMDCVQCDRCRLWGK
IQRTGYATLAKILFEINDADEFTKQHIVGKLTKEYELIALLOTFGRLESIESVNMFEKMY
KRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNSSQSHVFDLKM
PKAEIVPRPSNGTVNKKWKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCCGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACCTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTACGCTACGAAGGAGATTATCCTAAAAGGAACCTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTGCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGTTT
TTAATGCTAAGCTAGAGTTTCTAAAGACTATCCGTTATCTCCACCTAAACTTACTTTCA
CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATCTAC
ACTCCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGTGTAGAAAAAATTCTATTAAGTGTTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLLELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPDPYPYADGVFNKLEF
PKDYPLSPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAACCATCACTCATTCGGTC
ATTCTTACCGTACGATAAAACCAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCGGAGCATCTGTATTTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTATATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPMSWYLSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA
GTTCTGCAGAAATGATGTTTGTAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGATTTATC
CAAAGGAAAGAATTGTTATTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTCCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTTAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCGTAACTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACTT
CTTACGACAGAACCTTGTTGATTGCTGATTCTAGAAGACCAGAACCAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTCTTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACCTCCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCTAAACATATGATGCAAACTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTACA
GCTCAAAGGAAAAATTCAGGGCGATGCAAAAGGTAGTGAGTGACGCTTTTAAAGAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACCTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDAKVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGACGAGAGCCATTCTGTATCGTTTCGACAAAGTTTGCATGACTTCAT
GTTGTTTCGTAGCAGTATTCTGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTG
TTCTGGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTCCGCTGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCCCTTTAACCATTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCAACCATTA
CCGCCCTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATACCAATGATCACCCAGCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTTCTTCCATTCACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTCACAATAGAAAGAGCACCAACACGAAATATGGCTGTGCGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTTCCCAACATATAATCGCAATATTTTTGTCA
CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCAATTCAGACCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGCCCAAAGGAGCCCCAAGGGGCCCTTTTACCA
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTTACCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACAGTTGCCCTTAAGAAGTTATCTCAAA
AGGATATCAATTTTCATTCGTAATTTAGAATTTTAAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCTTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA
GTAGTGTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAACTCAACTGTGGTGGAAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCLLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLP SHFAFHD LK WFFHNR RAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDR TLISL SH
GNF SHQYNRNIFVTW WKS LFEASTAFRRASGLTVSPLTRRG IARFDHFRPVFNVS KFA SF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGG LNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETS A
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIALGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTCGC
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTACGATTTTTTAAGTTGCGTCTCAAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTC AAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAAC TTGAATATCATTA AAAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG
AAAGAAAAGTGC AACC TAAGCAGAATTC CATTATTTACGCGTCCATTTTTATAATGTTT
GAACTTTTGAGTCC TTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTGCTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACTTGATGTTATCAAGGCTTTGCAATCCCTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAAC TTGCCTGAACACATTTGCTCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTFLTEEGVEYLR EYLN LPEHIVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCTTCCG
ATTTTGCATAATGATCTTCAATTTCTACAATAAAAATCAAGTAGATACAGGAAAAATTTCC
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCGAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAATAGTTG
ATGATTCTGTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTTAG
AACATATCGGCTCTGTTTCATCAACTAATAATAAGTAACAATGCCCTAATCAACCACA
ACCTCTGTTCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG
CGAATATTTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGCACGTCACCTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGCAATTCAACCACACAGGATAATGGTCCAGTAGCAATGATG
GGCTGCGTATACCGAATCACTCGAACGCGAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTCAGCTGTAGGTGAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTTGA
ATTTCTAATGTGATGCAGAACATAACAATCTGATGTCTGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTTCGACGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTTCAATTATGGTGACAACAAAAGGCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCTATGGTTTAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATATGGTGACTCGTCTAATGTTAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACCTCCATGTTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAAGATGAAGACGTAGATGATTATGATCGCCCAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACCTTCCATTACATGGAAGGATGCCTTCAA
GATCAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAACA
ATAGCATTAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG
GATTCATTCGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTCCTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAATAACGACAAATCTTTGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAAGTACAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACACGATGTGTCACTCTCGAGTGTCAAGCTTTTAA
GTCTTGGGTCTCGTGAAGCCAAGCACGAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAACAATACTAATGAAAGACAAATACAAAAGCAAAACCAATGCTAGAG
ATGACAAAAGAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLSNNSNVVAPNPSIPSASTSTSPHLHREIVDDSVATA
NTTSNVVQHNLPTIDNNLMDSDATSHNQDHHWSDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKI IERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKKNINSKGKNERNDTSTKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNNKKKTSNNNGNNSNSASNKTNADIKNSNADLSASTSMNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNNNKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNLDELSSIKQEPHQLQQQQPPMDVQSVDSYTSNDPDSNVIKSPDKRSSL
VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNKRPLRTTVSKIFDSNPNGAPLRRYSVDPDHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
YNHKNDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSSRSNNNDYY
DFMVGNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKLQDQDVVVMDNVIS
SSDELIFDITVSAFNPGGFFSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETPKFQGGAFNRNYDVS SVSSVKLLSPGSREA
KHENDDDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
YEVFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGATTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAACTA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGATCTGATGT
GTAAACTCATGTGGTGCCTGGTGTGTTTCCAAGACTGCACTATTAAGTGGGAATTTT
TTTTTCTTCTAGTGAATTTTAAAAAGCGACGCACAGGAAAAGTGAAAATTTATTTAA
ACGGACGGCAAACATGAAAAAATTTACCAACCATATTTCTATTTCTTTTCCCTTTTAC
CTATTTCTTTTGAATAGTTTCTTCTCTCTGAAACGACAATAAACCAAACTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAATTTGAAATCCCAG
AAGGTGTTACTGTACGATTAAGTCCAGAATCGTCAAGGTTGTGCGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG
TCAGAAACTTTTGGGTGACAAGAAGTACAGAAACGTCCCAGTTAGAGATGGTGTACTA
TCGAATTTCTCTACTAAGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKMKRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVVPRDVTIEFSTNVKDEIVLSGNSVEDVVSQNAADLQQICRVNRNKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAAC
AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAGATAATGTATATATTTTACTATCTACGCAGTGAAAGAGTTCCCTTC
TAATGACACACTATTTACTTCCGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTATCATTTGATTCAAGTGTTCACATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTACAAA
AGGATTTAGATATGACCAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAGTCTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGAAGTTGGGAACCTTTAGAAAAAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQQRQIIKQALAQQKPLPKELAEDES LQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVMVRHDIINAG
NQSEVNPHLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKADADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTTCCACAACCTTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTTGTTTGGCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA
TGGGCTCAC TAGGCGTTT CATAATACGCGGAGGGGGAATACCAAATGCTATTGATTATGG
TTAAAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAGTATGTTAAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT
CAAAAAAGAGTGATTTT GAGCAGTATCTGTATGAAATTTTCATGTGTTGAGAAAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCTTTTGTATGAATGAACCAATTCAGTTACTAACTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGAATTGATGTCACCGGTGGTAAGAAAGCAGTAG
TCCTTTTGTGTCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAATGACCC
GTGAATTGGAAGAAATTCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAAATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTACGACAAGGTTTGGGAAGACATGGTTTTCCCAACTGAAATTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTGTGTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCAATATAGACTAATGCGTTTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTTCATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCTTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATTTATCTATTTTTTCTCTTGCAGACATTTAACACCTGAATTCGCGCTAACGCCA
GGATGATCTTGCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGACAGTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCCGGAAGGCGGTTCATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACATAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCCTTCTGTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAGGGCTTCTATTTCCCTCG
CTATCTTTCAGATTGTGCAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGTCTTACCACCTTACTGATTTTCTTA
ATAATAAACTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCCTGTTTGCCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIFYFYLVNVPKTRKTYCKGKTCRKHTQHKTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHHKAKTTKKVVLRLCEVKCKTRAQLTLKRKFELGGEKKQKQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTCTCTTGTTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTCCGT
AACATCCATACCTTTCTGTATAATATCTTGTCTGTAAAGTTTGTTTTTTTTATGAAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT
TCTAGTTGTAGATATTGTTAGATTAGTTTGAACATTGTTTTGATAACTGAAAAATAAA
ACAGCAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTCCTTACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGTAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACCTTTGTTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAAGCTGCTTACGGTGTGCTCAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTGTGTTGTTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTGCTG
ACGGTTTCTTGATTTCACTCTGGTCAACCAAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAAGAAG
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRRLINELTLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKSRTPKALPDAVTIIEPKEEPI LAPSVKDYRPAEETEAQAEPEVA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACATTATAATAAAGTCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAAGGAGT
ATGTGTCTGTAATTGAAGTGTTAGCGCGCGATTACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAAATTTT
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCCATTTCAAATATGCTTATTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTTATTGCTCAAGCACAAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTC AAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATCACC AAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTCGAGAGTTATATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTGGTAAGACCCCAGTATTGCTTGGCAGAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTACTGTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTAACCTACTAAGTGGCGGCGAAAATGAAGATTGGATGCACATATGCAA
TGGGCCAAGCTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTGATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATTAGAACTATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAACTCAAAGGCAAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTTA
ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTNTSGTIA SVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMAHYQSITKIKSILNGKYIITSGNDSRVI IWQTVDLVSASND DPK
PLCILHDH TLPTVDFQVSSSQGKFLSCTDTKLF TVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTL LL
IGDTEGKVSIAEIIYSKQIIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESK GKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDN KIDATSSLD SNAAKDEEITELKTNIEAL THAYKELRDM
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTACGTAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG
ATTACTTTATATAGTGTAGTTTGTTCCTTGAATGTAATAAAGACTTCTGTTTATTTTGT
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTCTTTTTTGAATAAA
GAATTTTCTTTTAAAGGAGTAACTTAAGCATTTAGCTGCACATTAAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGGAGAACATTTATTTTTTTTCGACCTTCTTTCCCAAATACC
CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATACCGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATTTGTTTGGTGTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGLTTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTTCATTTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCTGTATATCAGCATCAAGATATCATAAATCATAAATTCAATTATCTTCT
GTTTCCCCCTCTTGAGGCATCAAACGAGTGTGTGACTGATACACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAAACTGCTTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTTACTGTATTCGCATTTTCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAATGAGGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATAACC
GGAAAAGGGCTGGCTGTTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATTCCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCGTACGCTGGATCTAAGGTGTGCAACAACCATTCCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATAACGGCAACTCAAACCTCGGAGGTGCTCCTCAAGGTGGACCAACAAC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCTCAGGAATTCGGGGGCCAAGGTCTGTCAGGATTCAAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPMNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLSGVLGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSEDKAHKDLEVLVHKSILVVQVAKDSVVQILKNSAARWPRIWRSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA
TTGTTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACTCAATA
TAGTAAAGTTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTAAATC
AGCTAGTGCATACCAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTTTGGACA
CCAAATTGGTGAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAAACA
TATTCCCGGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTTCAGAAAGA
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTGGAAATATGTTTGCCAGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTACACATATCAGGATAACCGCCTACGTATTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTT
TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCGCAACGGCACGATTCATAGTCACTCTAGAAATAAAAC
TGAACAAACACAAATCACTTTCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCACCTGAATCTGTTCAACAAACAATACTAATTTCTGGGTGACTTACTCTAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPPFCLDTKLVLLEELQEGKQFNKNIFPEKALYLKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVLDLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPEP
VQQTILISGDLYSIALAVTSIESALITLDEL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGACACAGAAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCCGGTAACGGAA
TTGTGATAAATAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGCATGAAAGCATCGCCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACTACATACAAGAACGTTTTTTTGACACCCTTTACAACCTGAAGAAAA
TTTTCAAAAGTGACATCAGATCAACAAAGGGTTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTITLHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHWDQPIPLPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKII THEFALLA
NL SLNENLPLTLRELSTRVITSLRNNP PVVEFINESFPNFKSKIMAALSNLNSNHRSS
NILIKRYLSILNELPVTSEDLPIYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFFDTLYNLKKIFKSDIT
INKGFLNLWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTGTGTTGCATTGATATGACTTGTGTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGGCGTTTGTCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCATATTCAATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTGTAGAA
CACTGGTCCCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCC TAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTAAAGA
TTCCAGATTACTATTTCAGAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTTCAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRFTTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFFTIVTISSTNVGAAGKWTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCTTGGAGGAAT
CATAGGCAAAGAAAGAAAAGAAGTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCCCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGCAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGGAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTTCCAGTTTAGCCATTATCAGCACAAATAACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATTGACGAATTGAACGTTATTTGAATGACG
TTAAGTCCAACCTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTGACTTTGCTGCTGTTAGCAAGATTGAGGACCA
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGTCGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCTCAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTTCTCAAATCA
GTGATGCTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACCTGAAAACGGTGTGCGCA
AGGCTGTCATCGGTATGGGTGCTGGTGTGTCATGGCCGCTGCCGCCATGTTATTATATA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASALSQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTTCATCGCAAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTCTGTTTCAGCCGCTCGCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTGTGTAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAA
GGACTCCTCATTAATAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCAAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTTCGCCAA
ATTTGCAATATTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAGAAGATT
CTGACATCAAAAAATATTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAAGAACTGGA
TAAAGTTATGGCGCCAAAGAAAACACAAATAATGAAAGGCTGAATGACAAAAAAGAAAT
GGTTTACTTACCCAGAATTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGAG
ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAACGGAAAAAACATACGCT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAGGCTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTTC
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAAATCCAAAAAGCTGA
CAGATGTCTTTCCCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCTGTTTCAAGTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTTCGTACGCCGAAGATTTCAAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAACTTTTGTGTTGAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA
CAAAGTTTAGAAAAATCTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAAACTCAGTAGCTCGCTACGTCCCAATCAAGTTTGCAACCTCTGTAAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTTCTTTGATCCATCTGATAAAAGCAGTAGTGTTGATAATAGCA
TTCTTTTGAGGAAAGTTAAAAGTGCCGGTGCGTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG
GGGTGGAGTTGGGATTTTAAAGGTGTTTAAAGTGGAAGTTCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGCGCATGTTTTTGAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTGTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVNYTMEECYDDETDSEFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLKNSDIKKYFLVSKNGKIVRRDYPSTPVIIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFYTYPELIFSEERIKPLRYRGDDAPCTKEQKRKHKILQQKVGYPNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNIDFYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNEENLITYKSKKLTDFVPVSYPIPTFVVPVSKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKNTISDISSHISVDSYAEDFKRQGYIKKQFNTSNDISIPRKLTLGAQHRSR
KITGDIEKLQDDEKDRRECTKEKLLKIDIIRESLKSLLAIETLPKQNVSSQSSHGDIIS
SFKNALIGNSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFPDSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSSSFSTVNTFTGGGVGIFKVFKSGSSSGNKSSSRNSSSGDVFESEDDRNDKKKKKKK
KKSLLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCTTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCCGCCAAATTTAACGAAGACAGCGTGG
TTAAAATTCGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAACTATTGAACATAACGCAAGTTCAATATACATAAATTTTG
ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTATATTCTAACAGGTCCGCTGTTATACCTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGTGACCCAAATTTAATTGAAAAATTTAAAGAAGAACCACAAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAACCTCCATGCCAAAGGAACCGGAAACCA
GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTTACA
AGGCACGTC AATTTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAACTGCATAAAG
ATATTACCTATTTAAACAACCGTGTCTGCTGCTGAATACGAAAAAGGCCAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA
AACTATAGAATACTACCAAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGAAATTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAGAAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTTCAGACGTTGATCGCTGCTGGTATCATCCGGAAGTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTAD EYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLDGLDEAESNYKKALELDA SNKAAKEGLDQVHRT
QQARQAQPD LGLTQLFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRLMTIMATLMGVDLNMDDINQSNMPKEPETSKSTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPMEVDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEYKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTI EYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPEKAEAEARLEGKEYFTKSDWPNAV KAYT
EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQI AVKEY
ASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFPQGT SNETPEETYQRAMKDP EV
AAIMQDPVMQSILQQAQONPAALQEHMKNPEVFKKIQT LIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTTCAGTCCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCGAGAAACCCCTTCAAATGAGTTCCACTTTACGTCAGATC
GCATAACAACCGGTCATATATTTTTTTCTTTTGCTAAACCCCTACTGCAAGCACTTTTA
AGAAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTCCGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCCTATATAAG
AAGGGCGCACATCGTCCCCCCTAAGAAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCAATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCAGCAGCCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAATGCG
AAACCACGTGCAC TTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKD SCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEKC

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCCAAACATATGATATGGTATTA AAAAATGAA
AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAACAGTGCGCGCGGTAATTTTT
TGTCACCTCAGTAAGTAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTACGCCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCAC TTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCCTTGCGACTTGGTATATATCTTATTTTAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGGAAAATTTCTTCTCCAGAAT

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTCAAAATATCACCTAATCAAACCTACTAACATTTTC
CTTTTTTGTTCCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAGAAATTCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAGGTTTTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATTCCAAGTGAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAELRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGNGKIQKVLDDSKDVQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCCTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAATAATCACATCACTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAACCTACCACTTTAGCGCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTTTGTACCTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCTCCTCCTTGTCCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCTTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGACCCGTTAC
CCAGTACGTTACAGTCACCCCAATACGACTACACAATACGTTACTGTACCCGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCCTTGCTCCCCGTTTTGTACGATGTTCCCTAATGCA
AACACACGTCCTTTAAAGATCCCCGTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCTGTGTG
CGAGAAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACGTGTTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACTGGTAT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAATAACTTTAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACAGATGTT
TCAAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

CGGTAAACTGTTTTACGCGGAGATCCAACCTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAAGTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGTATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAACCTGCCAGAACACATTTGCC
AGGTACCTACATTCAAGAAAGAAACCACTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLEPHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT
GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTTT
CGGGACTGTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTTCAGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
CGGGCTTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTGTTCGCGATAGTCTGTCTAGCTCTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
CTTTCGCGCTCGAGTTGGCAACAGTACGAAGAAGTAACCTCTAATAGATAGATAAACCCTT
TTTGAGGGCATTAATTTTGCAGAAGATAATAGAAGAGAACCCTAACAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAATTTAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCCCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
GTTAATATCATTGTAGAAGTCTTACATGAGGACTATAGAACTACCATCCAGGAATTATA
GAGGAAATTAACGTAATCAGAGATCTATTTTGAACACATTCATTTACATGTAATGTCTGTC
AATAAAGCAATATTTTGAATATGCAAGTTTACTAACAAGAATAAATCTTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCGTCGTTTACCAAC
TGAATCCGTTCCAGAACCAGTTGTTTCAGAAATGAGAATTTTGTCTTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTTGTTTCCATCAACCAAAATCAACGAAGCTCACCAACCAAGGTCAAGAAGTTCCG
TGTTTGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATTCGAGTTGCTGCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIKSRVWYFLQKLHKVKKASGEI
VSIHQINEAHPKVKNFVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFPLPHRVQKSTKTFYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTCCGGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTCAGAAATACCTTACCCGCAAGCAAACTTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATCTCCGCAGGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCATTTGTTTTCCCAAT
TCAAACTCTTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAACTAGACT
ATATATATTTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTGAAGAA
CCGCTTTGGTTACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTGGTCAAGTCTGTTACTGAAGCTAACATTAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCGGTGCCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTAEVETIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCGCACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAACCTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCAATGGCGAACCAGGAAATTTGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAATCAAGTTTCTCTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATCTTTAGGT
TACGGGGTTTTCTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCATTTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAACTAATTGCTGAAGACAAGATATCCGATCTTCGCAGTTATTATTTCGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLSYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTTCATTTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAAT
TGTCACTCGACGCGCCGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCCT
GGGCCCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCCTTGGAAAG
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAAGTTATATGTGGAAAAATGGCATGAAAGTTTGAAGTGAGAAAGAACTAAACAGA
ACCAGAGTTCGTAAGATTTTAGAAATTTTATGGAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTACATATATCTGT
TACTACAAACCGTGAAATTGAAGCAGTTCATATACTTGGAGTATAGTCAATAAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTGTCCAAAGGAAGATGACGTTTCGTGATTTTCGTCATCAGAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA
GAAGCTGTGCGCAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD L AVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQQRKRHRQALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGTGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTATC
ATCATGCCTTCACTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAAGAAAA
AAAAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAGCGTAAGAAAGAA
GAGCGTGT'TTTGGGAAATAACACCACAGCATAAAGCTAAATTCAGTTTATATAATCTAT
AGTAGTCCATAGAAATTGCGAATAACGGAACAATAGTCCACCAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCGC
CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAAGCACC
CGCCAATTTCTTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAAA
AGACTAAAAGGTCGATTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATACCAATGAGAG
GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCCCTCCCTGCACTTGCAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGCTCTCGTTTGCCGTCGATAAATTCGAAT
CCGATCCTCCCCAACAACTTCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCCG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAAGCTTACTGAAAAGTCATCAGAAGGCACCATTAACGAAGCAAAGAGAGAG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAAAAACC
TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCTCTATTTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGCTTACCCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTTGTGATTTTCATCACCATTGCTCCCATTACACGATTGTTTTCG
ACAATGTAGCTTTAAACCAGGATATGTTTCAGAATAATTATTTCTGCTTTGGTAAACTCCA
CAGTTTGGACAAATTGAGTTTAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCCCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAATTTGTTACTG
ACGCTTGTCTCAGAGATCTCAGAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTCAATTTGAACAGCACTAATATTTGCACTTCTTATGATT
TAGCTTTGCTCTTGAATATCTTTCTAAGTTGCTTAACCTTGATTTTTTTGGATTTGAGTA
ATTTGTCGCAATGCTTTTCTGACATTTTACCCATCATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAGGAAGTAGCTGTCTG
TTTGTAATATTTTGAATTAAGTGCAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAACTAACACAGACG
GCGACTTGGATAGTTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTAGATTTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACGGACCATGGATTGCACTTTCCAGTTAGATGAATTGGATTGCAAGATGATTGCTAT
TCGATGGCTCTTTAGTAACATATGACCGCTGAAAGTGT'TTTAGAAAACTGAACTTGT'TAA
CGGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTCTGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACCTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATAACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGAAGGTGAACCTACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGTCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCAGAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLKYGKSRKTNTPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPD LKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDDNGSSSTQFVRKKRSTSISNAVVS SKPRLASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKT KRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDPRVKEISSPMRGVAPTAS KPTPILPSPALAVKDLSTVSLKRVSFVDFKFESDPPQQL
PSRTPPKGNILIPDDMISEVPSISVGISSSNQSAKSTNSNIKPLYTKKSKEYILALENQ
KLALREAAKHQQAHAFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKLCKFLLLNKSLNKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSQYINVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY
FILNSTNISTSYDLALLLKYLSKLPNLIFLDLSNLSCFPDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNILIKCKSLSHVSMTNQNVENFYLMNGTDSVPVQQTNTDGDLDSSS
TLDVKGQFAENLSFSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKD TTKRYLLKKYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNPNLNDVLGSSRD
DSKESVDSSSEDSKLPAKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFFVQQQRS LYPENESTRQTPFASGDTPI NTET
AGKSTSSPSVSTSNNETATTS LFS PANPKILPKIPSGAVLRS AIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVSDSV SAPNTDKGSVETLPAVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCATTCATTAATATTAATATAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAAACTACTAATCGTATATT CAGCAGGTCAGAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCATTCTAGAAAGATTT CAGTCTTCCTTTA
CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCCTTA
TAAAGCAAAACAAGACAATCACAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTAA
AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACCTTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTTCTTTT

CAGAGTGGGAGAATATACCTAGTGAAC TACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKS KRKKGSKKAAY
HRQPPEHEHTAPLIKQNK TITKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFPHPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEF SKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCCCTATA
GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCC TAGTATTACCCATATGCCTTTGTATACTCATATGCGAAC
TTGTCTAATAACAATGTATACCAAAAAATAACAGCTTGAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTGCGAGCTAG
AAAATTTCAATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCATATATATCATTTAT
CGCAGAAACTAATCGATTTGGGCCATTCTGTGCTCATTATAACTCACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCCACTGTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTGTTCAATTCTCATGGTAGCGCTTCCACGTTCCGCTCACG
AGGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACGGACCATTCACTCT
ACGGTTTTTAACCTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGAGCGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTTCCCAACGCAAGTGGTGAGCGAAGATTTCAAAC
CAAGGGATCCTACTGGTGGCACCAAGAGAAAAACAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG
TTTGTTCTCTACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCACTTTGGTACAATTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTCCCGAAGTGTTACCAAATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFYPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGV
HLTNGLKVYHVPFFVIFRETTFPTVFSTFPIIRNILLREIQIVHSHGSASTFAHEGILH
ANTMGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNCTKENMIVRTELSPD
IISVIPNAVVSSEDFKPRDPTGGTKRKQSRDKIVIVVIGRFLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKEIDFQQMIESHRLQKRVQLLGSVPHEKVRDVLQCQGDIIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDWMMKMANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGGATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTTCTATCGATTTACGGGTGAGGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTTCGCTAGAGTTTAAACACAT
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACAAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCAC'TTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTTCATAGTCCGGTGCATAATACGCTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGGTTTTCGGCCTGAAACCAC
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCAATTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCATAGAACATCAGAAAAGATCGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAATTTGA
GGGCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATCTTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGCTTTGATCAGGAAGATCACATTGATGCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAAATTTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTCG
GCAAGAGCAAGAAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAAACCAATAATTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAATTTCTGCAGCCCCGGCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACGAACTCCGGTAGCGATGCAAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTTCAAAAATGACGGTAGTG
ACTCTACTTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGATACAAAC
CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTACGGCAGTGT
TGTCGGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGGCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGCGAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLSNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTDEEVECFSEDNIEDGKVMNDKV
IAEHVMPPEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGETSPSSIETKLNATSVINEEQSKVTKEADIDDLSSHQNLRASLVKA
GDNISEAPYDKEKKILDVGNLTAAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDDSSFM
SLRRQSSKQHKLLNEEDLIKPDIDISSAGTKDIEGHSLLNYAPNMILSQSTGVERRFEN
SSSIQNSLNEIHDSGEHMASGDTFNELDGKLRKSKNGGRSQLGQNPINSQSTFPTIA
NIGSKDNVPQHNFTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNNQLLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQNSNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGMYHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTTATTTATTTATTTATTTT
GGATTTTATTTTATTTCTTTTTTAATGCTAAGAAAGTAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAAATTTCGCGCTCAACATGGCCGTATTTGTACATTATATCGTTCTATCATATC
GTATACGCCCGCATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAAGGCAAACAGTAGATTTATTTCCCTTCTTTTCTAGAAACATCATTATAACT
AACAAATATATAATTGGAATAATGGCTGGTTGGGATATTTTTGGTTGGTGTATGTTATCAC
CCTGTTACAGTTTTTTCGGATACTTAGTTTTATTTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTTCTAGAAGAAATTGCGTCCTTTACTAACTTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACTTTCGATTTGGGTGGTCATATCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAGAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCTGAAAGATTTGAT
GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT
GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACCTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGTTATTTAGAGGCGTTCCAATGTTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVFPFVILGNKIDAPNAVSEAELRSALGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTTGCCACCCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCCTGCGACAGCGCAACAT
CCAACCATCTAAAGGTATGGGTGTACTGACGATGCGATTATTTTATTAAAGTTCTGTCTT
TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAAATACAGAGAGCGACGCAAAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACCTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAAACATAGCCAAAGATGTCTGCCAAAGCTCAAAACCCATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMDLKIIEKLVNLISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKCKGTGVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTGTCTTGTAAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTTATTTCTCA
AAGTGATGCGAATTTTACAGAGAACACATTAACCTGGGGGCCATAAACCGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT
TTTCGATTTCAATTTGCGACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTATTAAATAGTA
TCATAAATTCCTTGTCTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAAACATTCCCAGTTGGTAGAGTGACAGAGATTGCTAAGAAAGAGGTAAC
TACGCCCAGAGAATTGGTTCTGGTGTCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAACAGAAATTTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTGTTTGCCAAACATTCACCAAAACTTGTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIPRHLQLAIRNDELNKLGNVTIAQGGVLPNIHQNLLPKKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCCTGCGATGTAAGAACTACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAAATAAAAA
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC
AGCCTTAAACGCAATCTCATTTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG
CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACTGGTAAATAGGGCT
ACAGATGAGCAGGAAAAACGTTGCCGGAAGTTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTACTCTGGTTGATCAAGA
GTGTTTCATCATTTTTTTTACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAACTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTTCGCATTTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPKQVYLSERIIDEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSE
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCEC
ASNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACCTCCACGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTCCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCGGCGGGGGGCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAAAGGGAAGAGATGTAAAAGCTTGGAAAAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAACCTGTAATTAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAATTGGTGACTATATTTGAAGTCACCCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTTCAATTAACCTCGCAGGTTACAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTCAGAGGAAAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCTTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELNDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTGTGT
AGCCTAATGTTTAAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCCATACATTACTTTTTTAAATATTCTTTTTTGTTCACCGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAAACTTGGACATAACTCATCTATAAGAAGTATACTGTTAAGAGAGGCATTTCATTTTC
GTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATATACAAAAATACGCGTC
CAAGATGTCTACTAAAGCCCCAAAACCCATGCGTGATTTGAAGATCGAGAAATTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTGAACAATTA
TCTGGTCAAATCCAGTTCAATCCAAGCCAGATACACTGTCAGAACTTTTCGGTATCAGAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGAAA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCTCATGAACAGACCAGGTGCTAGAGTCACTAGAAGAAAGAGAT
GTAAGGGTACTGTTGGTAACTCCCACAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCGTGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACCTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCTCTCATAGTTGC
TGTGAACCCCTTTAGTAATTAATGTTTTATTTTCATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAATGAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTACATTACACGAAAGAAAGAA
AGAAGCGTATTTCTTATAAGAGCAAATGTTGATAAGTTTATAGCAAGAATAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAAGCTGTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTC
AACTGTGCAAGCAGATTATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATATTATTGGACAACTTGATGATTGACGAAGAAT
ACCATTTCTTCAATAGATTCTTTGCCAATGATGTGAGTTTAACTGTTTCATGACGATTTCGCT
TTGAACATCTCTCAATCATTATCTCCCATTTATGGAACAATTTACTGTGGATGAATTACCTGA
AGTGCCTCTGACTTACTATATGAATACTCTTAGATGATAAAAGCATCGTTTTTGTTCAGT
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCCTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTTAAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTTCAATTTGATTGTTGCACTTTCTTGGATATCTAATTT
GGATATCACATATGGTGCGTTGGAAAAATCAACAAACCAATAAAAAAAACAATTA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDITISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEYPPFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPES
ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKNN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTCAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT
GTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTCCTCAAACCTGTATTTGATACTGCTAT
TACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATAACGTGCAA
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTATTTTTTATTTT
TGGCTGGTTGTTTCATGTTCAACCCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAATTTTTCAGAATGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTGCAATACTGTTCTTCGACGTATTTAAACGTAATAGCATTTTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCCTATCTAGCGAAGGC
AACTTTTGAACCTCCCCAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCTTTCCCTAATG
ACATCCCCTCTCAAACCTTTAGCTTAGCAGTTGTATTTAATGTCTGTACGGATAGTCAATA
ATCGTTGAAGGTTGATTTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC
TAAAAATGGTATGTTGGTGTGTGTGTGCTGCTTCACATTTTCAGGCTAAAAATGTTATCCGT
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAC TAGGCACGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCGCTGACGTGGGGTCTAGTTCCACTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCACAGGCCGTTAATGGCCTGAAACAGTTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTGTCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCCGCGGTAGCGTTCTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCCTGGTCAAAGGCGAAAACGCTACCTCGCTTTCAGTGTGCTTTCCG
TTTCATGACTTCGTTTCAAGCGGTCTCTTTTCGCTCTCGGTTGTAAACACACTGTAGCCTGCT
ATGCTTTTACCCTACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGCCTTT
TTTGCTCATTTTTCGTTTTGACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTCTCTCCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCGTTGTGCTCATCGCTGTTTCATATAATCGTTCGTCAC

TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAGCTTACATACGGAAAAGAGAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSMTSCTNALSFLFLLTLRRIHRHWYPYGAFL
LIFVLTLRWFRGPiAWVVVDVVFASCNVVFSPALSDENWPYVSFFGVVVIIVVTHI
GAFTACLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCGATATAGCAACCTTGTGTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACCTTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCATTACGGAGAGAAGCATTTCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCCTACCCACTGCTTGCTGTTTCTCAGTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTCTGATGCATACAATCTTTTAGATATTTATCTTTTAAAATTATTTTAAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAAAATGGCTCCATCTGGTATGTGAAGTGAATATTAATAGCACGAGAAAATTGAGAGGAAG
ATAGATGGGAACTAGTAGAGTTGATATTGATGAGATACGAAAACCACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTAGAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTCGTTTCGTTTCTGCTCAGATTCAA
GAAAAATTATCCATCCTCATTATACTTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTCCAAGTTTCCATG
AAAGCTAACAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNLTLPVNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCTAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTGGAAATTGTACTACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAACTCAACAATCTATT
ATTCCTAATTCTCAACAGGTGTCTGGGCCAACCTACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATACAA
TATCAACAGGGACACACAGTGTCTAGGTTCAACCTACATTGAAATTTCTTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTTGCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCATTTACCCTTCAACAGCAGCCACCACAACCAAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLLEYTLQVLVYRDDITKSTFELAI SPANLNISQRKIISILCNYLNLLLELFD
NGLIIIRKPGYIAQCITQQSIIPNSQQVSGPHTPQQHQQNQLQQQQQQHQHQHPSSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQOVQHQNQPPQQQQQQHVQPOYNYYNQ
QSIQSQPHSARPYQSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAGAAGCACGAACTGTGGGCAACAACAACAACAACAACAACAAAAAATTT
CTGGAAATCAAATTTGAATCCAACCAGCAGCGGCGGCGGCGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTTCTATATACACTGTTAAATC
AATCAACAATAGCAGGATATCCATTCATATACAAATAGATAAACTGTTTAATTAATTAATTAATG
ATTTGATTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAACAATTC
AAGCTTTAATTTCCACCTATCAAAATTCATTATTATTTTGTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTGGAAACAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCTGTCCTCTCTATCATCATTATCGTCTAGCCTCGGGCT
ATTCTTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAAATAATACTAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAAACCCATGTCAACACAAATGTTAATGCAACACAACAGCAA
CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCATTGTCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAATTAAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

TGTTTCGTGGATTAGCATTTCGCCAATTTACACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT
TGAATGGAAGAGAAATAGGTGGAAGAAAATTACGTGTTGAATACAAAAAATGCTTCCGGGCACAAG
AAAGAGAACGTATTGAAAGAGAGAAAAAGGGAGAAAAAGAGGTCAATTGGAAGAACAAATCGTTCTG
CATCAAATGCTTCTTTGGCTTCTTTATTGTTCAGCTGCTTCAACTACAGCAGCAACTAAAAAATTGGA
GTGTGGCTGGCACAATCCTTCTCATACCCTGAAAGAATGTTTTTAAATTTACCTTTTAACAATT
CCCTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACTC
AATTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCATAT
TTGAATATTTCTCAACGGAATAATCATATCAATTTATGTAATTATTTGAATTATTTAGAAATTGTTTG
ATAATGGGTGCTACTAATTAGAAAAAAACCAGGATCCATTGCTCAGTGATAACTCAAAAATCTA
TTATTCCTAATTCTCAACAGGTGCTGCGGCAACTCACCAGCACCACCATCAAAAAGAAATCAACTTC
ACCAACAGCAACAGCAACACACATCAACATCAACATCCTTAACATTTCATCATCGATGATGAACCTT
CATCAATTGGGTGGTACATTAGCTGTTCCAGCGCACCATGA

YBL051C_homolog_2 550aa (SEQ ID NO 288)

MDFRNLSTTPNQMGTVMQRRPSLSLSSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGNN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQLDSENNTKTDSNDASATNNNNVN
VMVNAANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNTNNSSTGSSNIANMLPSVSNATTMNNSNSINSTNNNTTINEADDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSTTER
MFLNLPFNNSFNPVEINFNDLEVLELYTQLVLYRDDITKSTFELAISPSIFEFSTENHINLC
NYLNLLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQOVSGPHTPHHHQKNQLHQQQQQTSTSTS
LTFIIDDEPSSIGWYISCSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:

95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAAGAAATACAATTAATAAATTTTCTTCTGTGAAAAGGCAATTTCCGGGCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAGTAGTTTTCAAAAT
CAGTTTCTTTTTCTTTTATATATTTTTTCTTACTTTCTTCTTCTTCTTCTTCTGACAGTATATTAATA
AATATTCCTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAATAACAATAATTTTTTTTTTATTCTTCAAGGTATAACAAGAACGTTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAAGCTGTGTGCGACAACCACTGACTCCTCCCTTAAC
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA
TTTTGCCTAAACCATCCCCTACACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGCTCAAA
CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAGAAATCAA
GAAAAATCAAAATCTACAGCTTCAACACCCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
AGAAAACTTCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTGTCTCAACATAAAA
TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAT
GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGTCACAAATCCAATCATTGAACTGGATGTTG
ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTTGAATC
AACACAATTTGAACCACGCTTCGCAACAGCAACAACCTGTCTGGATCGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTGCATTGTATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA
ATGCATCGCCAATTCCTTCTGTGACAAGTATTCAACAAAATGCACCGTTGACTCACGAAAATTCCG
ACAATTCCTCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA
TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC
ATTTACCATTTTTGCCAATAATAATATCTCGATCTGCCACCGAATTGTATCATAAATCTCAATTGC
TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAAGCAACCAAACTTTATATGTCGTTGG
CATCCTTAATTAACAATTAGCAATTGAAACATGTTGGATTAAACACCAAGATCAACTCATGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT
ATAGATTTGTTGGATTGGCAAAGAACTTGTCAATTACAATTAGGTCTACATCGTGGTGGAGAATTCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTTCAT
GGTTAGCAGTTTTCTTTTGTGAACAGTTTTGGTCATCATTGTTGGGGTTGCCACCTTCAATAAACA
CTACTGATTATTTATTAGAGAATGCTCGTGTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTTGGAGCCTCTGAATCGTGGTTCACCTAGTTTATTGGATAGAGAAATTGGAAAGATTAA
GATTTAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCTTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTGCAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTTTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTTGCAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAAATCT
TGCCCTTGCCATTTTACAACCAAATCATAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAAC TACTATTACTACATTAGTTCCAAC TGAAGCTATGAATCAAGCAAAAAC TGAATCTT
TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAAGCACCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAAC TACCGTTACCACAAC TATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAAAC TCTGTTGCTCCATTTGCATCTCAAATCACCACCTTTTTTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTGGGTTGGTTTGTATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLPQTKPVNSKRKSAASTPGNESKKSRSKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSTFCRQHKIKCNASDNYNPNPCERCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDLAKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENS DN SPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEF SRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLL ENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVYLYIKLMICCF AFLPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSII TRMRSHLTAS
LFYDLVWCVEHARRSVL DKGK RQAQPNKKILPLFPYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLLQQYPMQDQQQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTTCTTATCTACAAAAAAAATAACAACTCACTATAACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAATATTATCATTCATCTATATA
TACATCCCATCGATTCTGACATAATAGTATGTATGATCATACAGAGGGAAAATCACCTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTTTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCTTTTGGTATGTATTACA
TGATTTTTCCTCTGAATCTTCTCCGATCATCATATACTAACATTTTCGTGGGTGTTTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG
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YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIIYEEHKDEDGFLYVLYSGENTFGEKLAIIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

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CGTCCCTAAATATGAGTCAAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTCATTTTCCATTTGTTATGCTTACGACAACGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGCCTTATTGGTTGCCATATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGAATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTATAGTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAGAATTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGGTGCAGAAAGTAGTAAACGAAATTTGCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAGAATGGGGCATGCCAGATATCTATCA
AGAACTCTGATGGCAAACCTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCACAGCTAGTAGTCGGAACCGCTTT
ATGACGACTGTGCCGATGCCATCGCGTTGCCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAGTGCTTCGTCCGCATCAGGTTGAAGGTGTGAAGTTTATGTATG
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GTGCAGTGGTAAATAAGGTATTGGTGGTGTGCTGTACGCTTATTTCCAATTGGAGACAGGAGT
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AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC
TTGTGGCACATTTTGTATGAATCTCAGCGGTCAAGTTTGATTTGTTAGTGTGTGACGAGGGCCATC
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TTTTGACGGGTACGCCGATTCAAACGAGTTGGTAGAGTTTCACACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCAGCTAAAATTTGTTTACGCGAACTTTATAACACCTATATCTAGGGCCCGAG
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ACATTTTGTGTGTTTGTCCACCTACATCGTTGCAGCTCAAGTTGTTGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTTCCCTT
CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTTAAATTTGGGGATGGCAT
CCGGTAAAATAAACATTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTGACCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA
ACCCCGACATAAACGTATTTTATTTGTCGTGAAATCTGGCGGGATGGGGATCAACTTGGTCGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTTGCAATCGATGTGCGGAA
TTCACAGAGACGGACAATTGAAACCGTGTTCATTTATAGGCTATTACACACGGGGTGTATTGACG
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CGTCCAAATCTGATGTGTTTGAACAATGATGTTTGAAGAATATTTTGAAGATAGATACATCGACAA
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CCATAGAGGAAAGCGAACCACCCCAACAAGCATGGGTACTGTCATTAGAGCTTAAGAAGAAGA
TTGACGATGGTGAGGCGCTAAAGAGGACGGGTGTTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGATTTCTGCGCTACACCGAATTGCTAACAATTCAAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRPIKGGVAVVQVVKRKLPTTNPKPAKILTTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLLKQNPFMKEGAVVNKVLVVCVPV
TLISNWRQEFRKWLKANKLVNLTNNPMSNEKQDILNFGKLVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQORN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSLOL
KLFDYITNLKKFNQFEAFMINLFFKKICNSPSLLADDELFFKIVEEFNLGMAAGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLSFRLDGGSTPNVRSKLVNQFNTPDINVFLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGLKPCFIYRLFTTGCIDKIFQRLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

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TTGTTTGGAATAATTTATTACTTATTCAATATTTTTTTTCTTCTTCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACCTTCTTCAATTGGATTA
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ATTTAATTAATAATTAATGAATTTGGTGTACGGGTAAAGATGACGTGTTAGCTTCTAACTTAGAA
TTATTATCAATACTTAACTTATCCACAATCAGTTGGTGGATGTGGTATTACTCCTAATTTCTGGGG
ATTGAAAATTTGTCAACGATATTGTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAACATTACACTTTTTGGTTATTATTGCTTTCTATTATTG
GTCTTGTATCTCATTTTAGAAAAGATAAACGATTCTGTAACTTTTGCTTTTATCAATTTGCTTT
GGGGGGTTTTATTTCTTGCATCATGGCATAGAAGAGAACAACATTTGGTTAATGTATGGGGTGTTC
AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAATAATACCAATGGATTACAGATTTTTTAAACAATTGGCATTATCC
CCATTGCCTTGGTGTGTTGGTGTGTTTGGTATTAGTTATCAATTGAGTTGTTCTGTATTGAAATCT
TTTTAACCAGATTTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTAACTCA
GTGTATTTGTGCCAATTTTGACCATTTGTTTATAATGCTGTACGGATATTATTATTAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTAAAACCTTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTACCATTTGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTAATAACCACTATTGCCACATATGCTGGTGAATAATAGATTCTACACCAATACT
TGTTGAAATTAAAGAGTCAAGAAGAATTTAAATCAATCAAGGTAGATTAGATGCTCAATTTCTTTT
ATTTTCATTTGTACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTTGGGTTAAGAT
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCTGAAATATAATGTTGATG
ATGATTTTAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTTCAATTTAATTTTTTTTCAAGTTGGATAATTTTAAATTATTGAATG
GTAAATATTTCAAACCAACCAAGTTCCAAGAAGAGTTGATTCTATTTCATCCATGGAATTTAGCCCTTT
TCTTGTAGCATGGATTGGATCAATTATTTCCCCCGTGGTCACGGCATTTTACCGTCATGGTACTG
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TCTTGGTTTATTATTAATGTTTGTGTTTTCAGAACATGGATTTTTTGATTTTGAGTTATCTTTTATTGAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATATTAAATTGA
GACATGATTATTATTCTGGGAAAGTAAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAACATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLP IQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDL LYDKGF AAQIRPGDL DHL LVFVKLSS
YKFSEEA EKDLIKNYEFGVTGKDDVLASKLR I IYQYL TYPQSVGGC GITPNSGDWKFVTSIVPITN
AFNETT LVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVLF LASWHRREQHLVNVWGVQNSHLIEEHNSELAKVNERVEEKSTYFHANNNTNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGP GKSLLTLLPTVLISVFPILTIVYNA
VTDII IKWENHDNQYSKNNSILVKT FVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGR LDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRLSLKLPEYNVDDDFRGLVLQFGYLMFGPVWPLAPLVCIIIFNLIF
KLDNFKLLNGKYFKPPVPRRVD SIHPWNLALFLLAWIGSII SPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFK SQVEWENDFVDNDIKLRHDYYS GKVKPTY
KVHSD ELWEKFT PQSTL NFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399..1781 (SEQ ID NO 297)

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CTAACACCTTTTATTTTGTGTATACAAATTGCACAATCAATTACTATAACTTTTTTTTGAAACGT
GGGCTCTGTTTAGTTTAACTTCTGTAGTTTATTATTCCGATTGGGTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATCAATTCTAAATCCGATGAACCGAACACACAAAAACATCCAGTCTCT
GGAGAGATTTTCAAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATCAATTGAAG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTACCAATTTTCTTCTCTCCAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTGTTATTAACTAGTCAAAGTGTTTTCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC
AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAGTAATGGTAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAAC TACAAAGCTACTTTTAAAGGTGATTTGTCATTCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAAC TATGCTAAGGAAACTAGCCCAAAAAATCTGAAGGAA
CCTATGCCGGTACAACCAATGCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAACTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAACTTCAAAGT
ATTTGCTAGAGGGTTT TAGGTGATGATTATGAAGAAGCTAAACTGTCAAGTTTAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA
AACCAAAACCCAGGTTTGAATTTGACTACAAGTATGTCACAATTTATTCAAGTTGGTGTGCTTATG
AAATCAACGTCAGAGGAAGTTCAACATTCTGTGATTATTACCAATGAAGAAATTCATTGAAGAACT
CTTATGGTAACGATCTTTCCAAATATTATCTAATGGTGCTGGTAATAATTACACCAAGATGATTG
GTTCAAGTATTTTGAATTCATCCTTGGAAC TTTTGAAGGACACTAAGAACTCTAATCAAGTATGGT
TATCATTTGCTCATGATACTGATTTGGAATTTTCCATTCTGCTTTAGGATTATTGGAACAGCTG
AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTCTATTGTTCCACAAG
GTGCCAGAATATACACAGAAAACTTCAATGTGGAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTGCTGCCAATTCAAAATGTGCTACTGGTCCAGGGTCTCTTGTAACTTGATGATTTTG
AAAATTTTCTGTTAAAGAAAGAAATTGGAGATGTTGACTTTGTAAACAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCATTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQS VFQDVATPQQASVQQYNILNFLGGSAPYIQRN GYGISTDIPAGCEIAQ
IQLYSRHGERYP SKSNGKSLEAIYAKFENYKGFKGDL SFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGA AFRAKYGS LYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKT VKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNITYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNL SKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT
TTATTTAACGATGCAATAATTATTTCATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTGTAGTAACTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGATGACATGAAAAATACGTAGTTAAATTTTGTTCCTTGTTCCTTTATTTA
GCCACTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGGATTTAATTTCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTCATAAGTATGATTTGAACCTAAAATATC
AACTTTCATAATAAACATAATTCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATTCTAAGTGGACAATCTGTTTTCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTCCCTAGTAAAGGAGATGGGAAATACCTTTAATTCAGTGATGGAAGTTTTCAGAGATATGGTG
AATTTTCATGGAGATTTATCTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTATG
AAAAGGAGACTACTCTAAAAACTCAAAAGGTCCATATTTTGGAACACAAAATTTATTACGACATG
GAGCTTTATTTTAGAAAAAGATATCAATCACTATTTTGACCAAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCCTGGAAGGTGTTATCAAAAGTGGTGTCTATTTTCGCTCGAGGATTTTAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGTATTTCTCCATTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGTCAGGTAAATAATATGACAAAGGTAATTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGATTTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAAATTAGTTAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMI SRHGERFP SKGDGKYFNSVMEVF KRYGEFHGDL SFLNDYEFV TNP DY EKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSED TVEFVVVDED
KKMGGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGLDLSADQVSSLFLWCAFEI
NVRGYSPFCNLFTKDEFIRSGYRNDVGNYYQTGPGNMNTKVIGSPMVEASLKM LQEDSKIWLTFTH
DTD IEMYLTSLGLIVPPGDL PVD RVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYK LQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTTACTATACACAACCTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCCATCTACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAAACTAATACTGGTAATATGGAAATATAACGCCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAATAAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAATTTG
TTTCTTAAACAGCAACAACAACAATTGAAATTCAAAAATGGTTTCTGTTTCTAAATTTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAAATTTGATTCAAGACATGGTGAAAG
ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAAACAATTA
CGAAAAGGAAACTAGCCCAAAAAATCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTC AACATTACCAGTTTTCTC
TTCCAATTCAGGTAGATGTTACCAAATTCAGATATTTTGCTAGAGGATTTT TAGGTGATGACTT
TAAAGAAGGTAAAACGTGCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAAGAACGGAGCAGTAGTACTGCCAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCTG
TGATTTATTCACCAATGAAGAGTTTATCAAATATTCTTATGGTAATGACCTTTCCAATTATTATTC
TAATGGTGTGCTGGTAACAATTACACCAGAATCATTGGTTCAGTGATTTTAAATTTCTTTTAGAACT
TTTAAAGACACTAAAACTCTAATCAAGTATGGTTATCATTGCTCATGATACTGATTTAGAAAT
TTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTGCTGCCAATTTCCAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCACCTACAATGCTCCTTTAGGTGATTTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNGLLLAGQSVFQDVATPQQASVQQYNIVNSLGGSSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTFKGDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLEYKENSTLPVSSNSGRCYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVANSALTFRSACSKNKERSSTAKKYNNTYLNATERLVKPNPGLNLTSDVNNLFSWCAYE
INVGRSSPFCDLFTNEEFIKYSYGNLDSNYVSNAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA
TATATTTGATTGCGATTAAATGTCATAAATTTTAGTTTCGTAATTATGTCACAAAAACAAACAATCA
ACATATTAAATCGTTATCCCAACTTTGTGCGGTTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TGCACAATCAATTACTATAACTTTTTTTTGAACGTTGGGCTCTGTTTAGTTTAACTTCTTGTAGTT
TTATTATTCGGATTGGGTTAGCTCAATAACTGCATTTTCGTACAATAATGTTAATTCAATTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCTGGAGAGATTTTTCAAACCTTCTATTATAAA
TAGAACCTTATAAGTCCATAATAATTCAATTGAAGGATTATTTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTTGTTATTAACTAGTCAAAGTGTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
AACAAATACAATATACTCAATTTTCTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTAAGTCAAGACATGGTGA
GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTA
ACTATGCTAAGGAACTAGCCCAAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTC
ATGGTGTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAACTCAACTTTACCAATCTTCA
CATCCAATTTCAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAAACGTCAAGTTTAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCCTAGAAGTGCATGTTCCAAGAACAAGAACTGAGCAGTAGTACTGCCAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT
GTGATTTATTCACCAATGAAGAATTCATTGAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGCTGGTAATAATTACACCAGAATCATGGTTTCAGTGATTTTGAATTCATCCTTGGAAC
TTTTAAAAGACACCGAGAACTCAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACAGCTGAAGATTACCAACATCTTACATCCCATTCC
CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
GTGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTGCTGCCAATTTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACCTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHRGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAAAGTGGAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAGAAAGAGCATA
AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTTTAGACTACGTAAAGTACTTTTCGATTCAAGGAAAACCAAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTAATCACTGAAAACAATAAACAT
GCAACAAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTTGTTTCA
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAAAAAGAAATGGGTCAAGAAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACTCTTGTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAAGTTTGGCT
TTGTCCTATTGTTAAACAAGGTGACAATGAAATTTGAAGGATTAAGTACACCACTGTTCCAAAAAGA
TTAGGTCCAAAGAGAGCTAACACATTAGAAAATCTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTCTGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA
AGATTACGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNI SYPANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCI VAQDL SVLALSIVKQGDNEIEGLTDTTPVKR
LGPKRANHIRKFFGLTKEDDV RDFVVRREVT KGDKTYTKAPKIQRLVTPQTLQRKRALKAKKV KNA
QQQRDAAA EYAQLLAKRLHERKEERA EIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGATAGTTGTTGGTGATGTTGTTGGGTTGGTGGT
TCTATATTAAATGGTTTGTGTCGCTTTTACTTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAAATGAGAAATGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTACAGAGACAGAAATATTAATCAAGGATCAAATTTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTTATAAGTATTTGTAGTTGAATTTAAATTTTGTACCTTAAAGTCTTTTAAATTTAAT
TTTAATAAAAAGTGGTGATTTGGCAAACCTCAAGAGTATATTTGGTGAAAAAATAAATTTG
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTACTACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAATTTGTATATAAATCTGATATCAATTCCTTAGCATTATGCA
CTGATTTCAGAACTTTCAAGTTACGACAAATGAACCATTCCAATACAGTCTTGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTTCGATTTGTTTCACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAAATTGATAAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATAACAAAATTTTGCACATATAGAAAGTGAGA
AATATCAATTGAATGATTTAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTTCCTATTGAATTGGAAAACCTAGTTTGGCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCCAATCGAAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAACCTATGATGAGTTTATTCCATTCATTAAAAAGTTTGTTCCTGCCGGTAAAAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNLKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDMSMVT
SIIHKFTIESEKYLNDLKITQWFGIVEMSKINHMTDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTTCCTATTTTAATTTAAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTTGAAATGGGGATTAAAAATGGGGATAATTTTATTTTGCCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCCTGATTCAAATTTATGGTCAAGCTAAAAGAGAAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCCGGTGAAATTACCTTTAT
TTGATTTATTTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCCCTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCATTCGCCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAAAAACCATTATGGAAAGACAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTTCATGATGATGCATTGAATGATTTGTTTGATA
TAACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIALSFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWSFVDDDALNDLFDITKKKYKLSIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAAATGAGGAAAAATGAGGAAAACGAGGAAA
ACGAGGAAAAATTTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTGGTCAGAA
CACAACCTTTGGAAGAAAGAAAAAACCAGAAAAAGAAATTCATCTAAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCCGCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAAACGGCCTTTGTCCTTGGTTTAATTTTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTTCATGCACAAGCATCAGACCAACAACCAACATAACACCAAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACTGATGACA
AAACAAATCAAAAAATATCACAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACATAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAAATATGATTCACCAATATCTGATTTGATAAAAATTAGAT
CATTATCACCAATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTGTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDNTNKDTTKVKPDNGEYDPI SDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTPVNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCCTGGAAATAGCCATTGTTGCTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTCAAAGTGCCTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAAAAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAACATATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTCACGATCATTC
AATAACCAAGAAACGATAATATTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA
TAACATATGGTCATATACACTTTTGAACATTTTTTACTAACAATTTACTTTTGTTCCTAGACTTTTGTT
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAATTAAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAGAAATTCGGTGGTCTGTTGTCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLVADSRREPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAAAGTACTACAGTTCAGTGGGGTGAATACCTAAATAG
GGGGGTAGAAATACGAACTCCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAACTTTATATACCTCCACAACCTCACTTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAACTGCAAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCCACGTTTTAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCTTAAAAAGGATGAGGCTACAGGTTTAG

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNI PDDYLSDILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)
CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAACTGACTGAGTCGTCTCTCAACAATTTATTCTCCTCGTCTTATT
TTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
MRDKWRKKRVRLKRRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCCTGGTGTTTTCTCACTGTTTTTCTTTTTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCATTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTGTTGGGTTTAGATTACTA
TATTTTAAAGAAACATATTATATGAAATGATAACCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAATGAAACATTAAATACATACTAA
CTTTTTTTTTTATTTATTAGGCCGGTGTAAACTTTTCGAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACCTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)
MAGVKTFELRTKSKEQLESQLEVELKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLTKEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)
CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTAAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACAGTTACATCCCACAAAAATCCCTTAATCTTGTTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAACCTGGACTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCTACTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTGGAACTTTATACAAAGGATCAAACCTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTCTGTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTC AATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCAACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTGCGACTTGCCAACTTTTCTTCCA
CACCATCACCATCAAAAGCTTCAGCAACAACGACGACGACAACTGCAAAATGTCACAGCCATTGACG
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AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCTAATGTATTTACAAGACCTTTTGTATTCGG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCACCTCAGTATGGTGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAGGATATC
AGAATGCGAGAAAATATGGTATTTCAAGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
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TGTTTGATATGGCCATGGATAAATGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTATCTTGTGGGTTTCCAATTTCCAGAGAAGAACACACTGTTTTCAGGT
GCTCTTTTTCGGCGAGTGGCGTTTTCAGGATGTTTTTAAACAGTAATACAGGCAATGCCAACGGTATG
GCAATGTTAGCGGCAACCACAACCACAACCACAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAAACACCATACATGGTCGTTCCCAATTATAACAATAGTGTTT
CATTTAGAGCAGGTGACTGGAAATGTGAAAATGTCATGTATCACAATTTCCGCAAAAATTTGTGTT
GTTTAAATGTGGTGTGCGCAAACTGCTATTATAACAATCAACAAAATAATAACAATTCATTTCGGTGA
ATTC AACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAAACTTGAATAATAATG
CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGATGTATTCACAACAATTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFVTKDSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHII SKKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTS LTNII TALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNGKVIANLHAKIAKLIKKSIPVENHPNVFTRPFDSAQDITAFTSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSKVFDMMAMDKLLLTSPFLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPTGNVTNHLNNS ETNLNNTNLNNNNHHSNNYHNHYHHNNNNNNHGNNSNGNTIH
GRSHYNNNSVPFRAGDWKCENCMYHNF AKNLCLCKGVAKPAINNQQNNNTIHSVNSTAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSQPQGHYHNSRNNNASGASKFNNGYNPKNQYNNNSKNLSNNF
GLNGMHQQNQNLILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

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GGTTATATTTTAGCAGTTTATAGACAGTGTATTCGATGGGTAATATAAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAAATCGATTTGAAAAATATAAAACCATACAGCTAAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAAAATGTTGTCCGCCAAAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG
ACTTGTGTGATGCATATAATCAGATTTGTTCATGCCTTCCAGAAAATAAAGAATTGAAAAAGTTGTTGT
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ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACTTTAGTTCCTAATGTCGGTCAATGTTTAG
AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
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GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
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CAGCTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
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TTGCTACATTGGGTGATTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACCTATTAAAGTTACTTCGGCTGATACTGGTGTCACTTTTGGTAACATAG
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TGGATTACATTAAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAAAAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGCAGTAATTGGAGAAGAATGTCAATTTTTATCAG
CAAACCTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCAATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFNLLLEKGDVVDKDDTMKKILITILNGDPLPDLLMHIIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVFAWLSIHKVSDDLAPDAELIYRFLYEENDSVCKRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQOYAQLMTEIISSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNNDVKIITLERINQLHKQHPVLQDLSLEILRGLSSQDLD
VKKKALDVTLOFITTRNVEDVVKLLKKELOSTALSNDKKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAAYEVITFVKEVVEKFPDLRDAILRLILALPHVKSGKVFRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASSELKSKRRDDTEESQEEETEYDGKPRRKGPPVLPDGT Yates
TSETTDSLESKTPIRKQILAGDFYLGAVLASTLVKLILRLQLSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEEALA
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EAFVKVHQYDVVLDVLLVNQTTTTLRNLSVEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDGHSDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELKMGTMQCLTPGAVIGECCQLSANLYSRSSFGEDALANLCIEKQSDGPIIGHVRI
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YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

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TGTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAAAAAAAAAAAAAA
AAAGAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
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CTCGGAATTTCACTGAATTCCACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTT
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AAGTCATTGCCCCCGTGACAATACATGCGGAATTGAAAAAGCCTGTTTTTATTTTGAATGAAAT
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AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT
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CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAACTGACCCGATACTATCCAAACATTTACAAATTATTGGTGATC
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AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAGAATGGAGTGACCAAGCTCCAGGTGATACTG
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TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVTYQLLKL
YRVLRGYGIIVDSIRRLYLIVSVSTVSSQIFSLPFIKSKIDKELQATIGKVEEIEIMKNDPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPVGV
RKMEAEEVHMLVDIFNAPSDGCGSTTSGGTESLLLGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSIIVSFLEKSKVHGDRKLPIFDRLPGVTSISCDTHKYGFAPKSSIIIMYRSPKLREC
QYYIASDWTGGMYSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKVRAIETDPIL
SKHLQIIGDPIGSIIVSFQLAQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTPVPVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
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AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTTCGAATAGAGAAAA
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AAAACCTCCTTTTCTGCTGATAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
CTACTCTCTAGACAAAATCAAAACCTCGAATATATTTTTTGGTGTCTCTTTTTTTTTTTTTTGCCT
CTCGTTGAAATCATCTCCATTCTTCTTTCCACGCTCTTTGTTGAAAACCTTTGCAACCTAAAAAAT
AAGAATCACTCCAACAAGTTTAACTACATTATCAATTATGTTGAAAACCTAGATTAAACAAAGCA
GGCCATAAGTCGGGTTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT
ACCCAGTTGGTCTAAAAATGTCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC
TCACTGCTGTATCATTAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCAATG
ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA
TTTTAGAACATACAACCTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAATGA
CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTGTTGAACCGC
AATTAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAGGGAGTTGTATATAAATGAAGGGCCAGTATTCGAACCTGTCAT
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGTGATCCCA
AGAAAATTGTTGATTTGCTGTACGAGGGTTACTAGAGTTTCACCTGAAAAATTATCATCCATCAA
ATGCAAAAACATTTACTTATGGAATAATACCATTGGAAGACAGTTTAAGTAAAAATAAGCAAATACT
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CAGAAATCTTTGATGTCAACATCCCGGGTCCAGTTGATACAATGAATGGTAAAGAGACTTCGAAC
AGTACTGCACATCTATCACCTGGAACCTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT
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CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTAATGAAAAAGTTATGG
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ACAAGAAGGCAATCTATGAGCAAACTTGGAATTAGCTAAATTACAATTGGAGGATCAAAATACAG
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GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
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TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAACCTAAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA
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ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCGGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAAATTTGATAAGGATATTTCTTCGAACGACCAA
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GTGAAAATGTCCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTGAACGGGA
CATTAACCTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTC
AAAGCGTCGATGCTCCAATTAATATCTCTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTGGGTACCCTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSRASRVVRRYACSHPI SPNLDPVGLKLHGVEVTQTSPPIPEFSLTAVSLKHTESGA
THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNMT
GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYIKFLESITYPSLNNSGGDPKKIVDLSYEGLLFHSKNYHPSNAKTFTYGLPLE
DSLKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCT SITWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK
VDNFNEKVMETIINNKIIPELSNEESSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTFVLP TLTIDDIPKRGDFY AIDLQGVNKKVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDDEVLEKLSVLIKNMGQNQINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIVENEKLEIKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSKDGASLQILSQLYSFKNLHHSKIRESNAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRSDLSYGLDANWNDKDLQEA KLRVFSVDAPINISSQGASAFFENIDDLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNWKQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAATGTTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACCTGGTTTGAG
TATTGGAGAAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAAGAAATTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCCTGCTAGAGGTTTTCTTTTTGTATGCTCTGTAACAGTGCGACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCTAATCACATAGTTAATTCTCAAA
CTTTCTCTCTTTCTCTCTTTGCTTTTCTCCTAAGGAAAAAAAATTTATTTTCATTTGTTGAAAAT
TTTTGTATAGTTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTATCCAACACTACTGTTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA
AAAAACTTTTTCAAGAGATGGATATGGAACCAAGATTTTCGATTGTTATCAACAAATATAAAGAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTTAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT
TTTCCCTGTTTAAAGTATTTCGATTACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAAGAATTGTCACCATATTGCAAAACCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACCTGGAATCTAAATT
GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTCGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
ATAGTTATTACAATATAATAAAGCAAATAAAATAAAGAAATGATAAAGAACCATATTAACAAAGTT
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GTAATACCTAATCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTCACACTAAGTTAAGGAGAGTGCAGAAAATTTAGTACTAACAAAATTTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAATTTTTTTGAAAAAAAAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTCATCAAACTGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACATATGAATGG
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AAAGAGAAATAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAACTAGAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCAACATTTT
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ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAAATCTCACCATTCCCACATGCCATTGTTGGTGGTATGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACATAAGTCAA
GCCATTTGTTAAATTAGTAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACCTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAGAAGGCTTTTGAAGAAAACATCAAGCTGGTAAGAACAATGGTTCTTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVIVKPHDEGTKSHPPFHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKAFEEKHQAGKNKWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

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ATTCTTTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA
CTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTTTAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAAGCTACGAAAAAAAAA
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTTAGAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAGCA
CTGCGCCCAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGCTTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGAAGTCGGCACTAAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAGGATCAGTTAGAGAATCAATCTTGAATATGACACAAGCTTCCATGACAACAGATAACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTGATTGATAAATCAA
ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG
AACACCAGAAGAAGCTCAAAAAATCGCAAACCTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDIAIKGIDERVGS�DVKLSKINSELSTYQQKISRMRDGPGRSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTNDLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELEALSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTTTACTAAGGGTGCCTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTTATTTTAGTTT
TTGGTTTTCATAAATTATTTAAAGAAAGCAAATAATTATTGAAATAAATTTATATTTTTTGGTTTTT
TTTTCTTTGGTTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTTTGAAAATTTTTCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTATTATTCATCCATATTCTTCAAGTTAAAAATAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAACACATCAATTCCAACCTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTCCAAGTACTACACGTCTTTAT
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CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
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CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAAATTATTATAATGAAATTATTAACCTCATCCTAATGTTTTGAGAT
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AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGTTATATTATTTGCCCTTGTGACAGGTA
GATTACCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA
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CGGTATTGCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACCTCACCAG
ATGAAAACCCCGAAGACATCAAAACATGAACAAGCCAGCGTTACGAACCAAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
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GTCATAGAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCCTCATTGTAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTTCGTGGTAACAATTCAAGTGGTCATGATGATA

GTGTTCCACCACCACCGCCAGCTCACAAAGGTGAATAAAAAACCATTGGATGATAAGACGAATTTCC
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AAACCATTTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG
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CTGCTGCTGAAATTAGAAAATTCAACACCATTTTTACCTAAACATGAAATGTCTACTGCTTTTATTG
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ATCAAAGAGATTTTAAATCAAAAATCAGAAATTGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLKKTLLGRGATGRVLLATHQTTGQKAAVKVSKSELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVREARDL
IARMLEVDPMRRISTEKILRHPLLTYPMSNEDLISEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI
LWNRPEEEIVDCLLDKGSNPEKTFYALLMRYKHNDQDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYK
SPSKRYSYNQSPKSPYGRRSNSQRFENEPLKAKPRNIYNEIVDAQSNFSLPSPSLPSPKSDR
YMIDEPNQPLQOPALSQVPENPIVDESPDLMSAKISSGKRNSIIGKNNNNNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELEKARRLEKKRRQKRSILSSKKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPVKRRQTPVLTRRPVSRDLPL
WQAHENEQLDRAKDALEQEWDRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE
RERDYELPEPTVEDSNLTDYMTETIRKSRLNSQLNVRDPLNEKRKSEPKTLISNVQIPSVTRKSR
NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENQEQHQNMMNKPALRTSIADRLDKAGLAEPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSEVHKRQYKSMVSESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPLHNGGIESSQPMKVRGNSSGHDDSVPPPPPAHKVNKKPLDDKTNPFPPEVDPKRKGSGF
FRKLSWGSKKTIENNTNAATNTTTQOQLPSPAESKEEKPKSSFRRWFSSNTPSAAEIRKFNTILP
KHEMSTALFALLNSWSNFGDKDLRNDQVGYITGAISKHNSFNLKSKFKRIKINQRFNQKSEIVC
VRVKGSKVTTDTLFCIEIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

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TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
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TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCACA
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CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRKFEGRQPANTKIGPKRIHSVRTRGNGKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACACCACAGCAATATAGCAA
TCATAAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACGTGCAAAATGTCTGACGCCGGAAGAAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGGCAACAAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACGT
AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTTC
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTTGAATCTTGTTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACGTGCAAAATGTCTGACGCCGGAAGAAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGGCAAGCAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGGAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAATACTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAACAAACAAAAAGAAGTAGTAGTTTTGAAAATGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATATGAAAGTGAGTGCACATAATGTAGAAAAA
TGTGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTGCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCACACAATTATCAAAACAATGTCCAATTCAGCAGGTTTTGATAGAC
ATATCACTATTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATACAAAAAGAAGA

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTTAAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGTCTGATGAAGGTAGAGGTCCACAAATTTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAAGTGAATTCAGAAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGTCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAACA
AATTAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAATAATGAGAGAGAATTACAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCGAAATACTAACATTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTCTAGAGGTGACTCTAAAATTTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCCAACAAAGAAAGAACCAAGAAGAATTTCTTGGAAGTTT
TGTAACAGAAGACACCACAAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTCCGTGCTTCTTTGGAATTGATCAAAAGAAAGAAGTCAAAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAQKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATACCCTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCTTGATTCTT
GGTAACAAAAAATATAATTATTTAACAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCTTTGCTTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTTCAGTTTCAGTCTAAAAAATTTTTTATTTATTGTTGTTTATACTACCC
TTTGCATATATTACTAATATTTATCTTACCCTTTTCATCATGGATACAAAGGAAATAAGATCTACCG
TATCTAATCTTGAAGAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTAAACCATCCGAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTTAGTTAAAAAATGATCAGAAATTTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCCCATCATCATCGGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGTGCCCGTAAAGGTCCAAGAAATCCAAAACTGACGGTGTAATACTCAATTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAGCACAGA
AGGTCAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNLDGVKPSKLLRETQVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSIAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPRLRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAGQATEKRAVTDR
FTCGKCKHKVSYQMQTRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATACTTTCCAGTTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTAATGTTTATCAAGACTAAAGTTCCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGCTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAAAAAAT
AATACATGCAAATACTGCATATTAGAATTATAAGGGAATGAAATGAAAAAAGAAATAATTT
TGTAAGTATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT
TTGAGTTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAATACTAATCGAAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAACTTATTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCACTTGGATA
AATACCATCCAGGTTACTTCGGTAAAGTTGGTATGAGATACTTCCACAAACAACAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKRGVNSAGKGRIGKHKRHPGGRGKAGGQHHHRTNLDKYHHPGYFGKVGMRYPFHKQON
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLPEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)

GCTATCAAAATCACTGTTTCAATGGTGACAGAAAACACGTTGCTGCTTTAAGAAGTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGCTACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAATAAGATGGTCAAGATTACGTTGAAATTAGAAATTTTC
TTGGGTGAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGGAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKS LIANLITGVTKGYKYKMR FVYAHFPINVNI IKKDGQDYVEIRNF
LGEKRVREVKIHEGVTMEISS TQKDELIVSGNSLEAVSQNAADIQQICRVRNKDIRKFLDGIYVSE
RG TIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAAATTGCCAGT
TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTATGAGTTTTGATTTCTTCTGATGTTTTTTTTTCTTTGTTTTCTT
TTGTCGTTGTAGCAAGAAGAAAAAAAAAAGTGTCTTCACAAGCTTGGACTCAATTTTACCCTT
CCACAACTCAATTTCAATTAACATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATCTTGGTGTAGCTATTACCAATAAGTTCACGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCC TAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCAATTTGAAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTCAATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTAAGGAACTCTTCTTCTTTCCCAAATCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTCTGTTTCGAGTGATTTGGTGACCAGTAGAAATTTCCCAATCGACGTCTA
TACCTAGGGTGTTGGCATTTTCCCTGGTGGAACCTTGTGGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGTCTTTGGCCACACCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTCTGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCTGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVS VSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSS TLKVTL LAFACFN SIIFRYYINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFPNSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLA FSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATP SHSAKSVVGGFAHQWILGLSFDEEGKHLASCGFDK CIRVWNLET SEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCATTAATATAAATTTACAAATCT
GATAATAAACTACAGTAAC TATTATGCAACAATTGAAAGTATCCTGTGTCACGTGATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTTCTA
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGCATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAAATCTTTCGTTTGAAAAGTTTGTAAAGGTTT
GTTTTCTCAATAGTATATCCATACATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
GAAATGTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTCAAGATTGGAATCAAA
TTATGTCAGATGTGAAGAAGACTAAATATAACAAGAAGTTCAATCATTAATAATTTTATGTAAT
ACAACGATTATCAATTACAGTCAACGAATAGATAAAACAAAAGCCAGCATATAACAGATACGAGT
GATTCATCCCAGTGATATAAATAATGATATTC AATTAAAAACAATATTAAGACATTTTTTATTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTAAACATTTGTGTTGGTGAATCCGGTGATAGATTAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAAC'TTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG
AAGAAATCTTGGAAGAGGTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAACTTCTCTGCTA
CCGGTAACTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAAC'TCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)
MSDKSQNVRELRIEKLVLNLCVGESGDRLLTRAQVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGKIDPSIGIYGMDFYVVMG
RAGARVTRRRKRSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)
TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCAGCTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCCTAAGACGCTGTCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCCAACAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTCTTACAAAAATTTTTTCTTCTACTTTTTTCAAGAATCTTCTTTTA
CAATTTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAAC'TCTGCTAGAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTTGGAAAAAATTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAAC'TTTGTTGACGAAAATGACGAAGTCTTGTT
GGCTGGTTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGGTAGATTCAAGGTTGTTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAAGCCAAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)
MGKGKPRGLNSARKLRVHRRNMRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKKVTAFFVNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVS
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)
AATTCATTTGATCTCTAAGAAGATGAACAGGCC'TTGAATGGGAGGGGTGGTTTCGACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAGAAAAACC
ACCAAACCCCCACCACCAACCTAACCTTTTCCCTTCCATCCATTCTCTTTCCCTTACTTTGCAATG
TTGAATCCAGTTATATTCAATTAAGATCCTATAAAATACGATTATTCACAA'TTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATTAATCAATTAATGTTTAAATAATTTGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAACTTGTCACTTTTGCCATTGTCAATAACACAAAATATCAAACATTGAAAT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGTCTTATAATGATGAGGATGATAAAATTACTACT
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTTGATCATTTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTT'TTAACTTCAAATAAATTAATTTATTGGTATAACTGGT
TCTAATTTATTAAATTAATAAAAAATTTAAATCTCAATTACAAACTTTTAATCAAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTGAGTGAAACCAGTGTTATTTTTTTGAAATTTATGAA
ATTAATGATGTTTGTGGTCCAAC'TGGTTATTAATTAATGATATTGATAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAATTTTCGTAAAGATCATGGATTTAAAT'TATTAGATATT
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVFIKDPFIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLOTFNQRLVIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIKVIIGNIEENSWKGLSSTDIREQEYNRLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTGCATGGTATTAGAGAGTGGGTGTTATAAAAGAA
GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTGCATGATTGCTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTCTTTGTTTGTGACGTTGACATTTTTTTGCTGTTGTTGTTGTATGGGAATT
TTTGATATTAGTTGTTCTTTTTGTTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT
TGTTTTTCATATTTTTTTTTTCAGAACAAGAACAATAACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTGGGTTTGCCATTATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTATATCAGTTAACAATGTCGTATCGTGGTCCATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATACGTCAGCAATTGGTAGAGCATTTTTGGTGGCCACTTTCTATGAGG
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAAACTTGTCGGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCTTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT
TGGGATTCGTCCTTTCTCTGATGTTGGTCATTGGGTAGAGTTTTTCATTATTATAATCGGGTTAACTT
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATTTCTTCCAAGTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGNPQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYLYHNRYRHWRLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFLSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFFSSDWSLGRVFIIIIGLTSCASIVVGKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLLVNAGAGEFSIDEXKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGCTATAGAAGTAT
TAGATATGTCTGCCATAAAAGAATAAACTAACTAGACAAGTGTATAGAATCTTTTTTTATTAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTCATACCAATAAAGAACATGTCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGTCTCCAAATACTCTGCCCCAGTGGTGGTCCAAATTGAACCAGTTGGTC
GTTACTTCTTAGCCACGCCTCAAGAACTTTGCGTGGACACACTTGGTCTGAATTTGAAAAATTTGG
AAGCTGAAAAGAAATGTTAAACAATCGAAGTCAACGAAGATGAGGATTTGGGAGATGAAGAACAAA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTTCAAATTTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCCATTGTTGGGAAATTTAGAAAAGCACCAAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCCGCAAGAAGCCCGCTTTTGAAGCCAACCTCAAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTCTTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAISKYSAPVRRPIEPVGRYFLAHASRTLRLGHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHPREWKTANLYAVLGLSHLRKATEDQIRRAHRKQVLKHPDKKSASGGL
ENDGFEKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQVPV
LLGNLESTKEEVDAFYFSWGRFDSWKTPEFKDEDVDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIEVERAHAEDPRIKLFKEKAKKEKAACKWEKESGSRKAAEEAAKKAEEAAAKKAEEAAALK
ANSKKAKEAAKAACKKNKRNIRAAVKDNVYFGDSAKSADIDADVLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTTGGTAGTAGAAGAAATCAACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTCAGTTTGTAGTTT
TGGTTGTTTACAAATTGAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGACATTTGTACACACACAAAAAATACTAATCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTCTCTCTTGCCATACTATCGCATTTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAAGAAAGAGAAAAAATAATTTTCAGTTTCAATAGATTTT
AGTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTTACCATGAG
TTATGGAGGGATATTCTTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAATTTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTATTACTGAAATCATCGAAACGAATATAACCCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTAACTATTATTTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAACTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTTCAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSATEAKQHKLKLTVQQPRSFMDVKCQGLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATGTTTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTTTGTTGGTCCCTTCTTTGTGTTTTGATATTTTGCAGCTGGTCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGGAAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAGAGCTGGAAAGTGTGATTAACAACAACGAGGGAAGAAAAAACTTAA
TTAGGTGAACAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCCTAGTAACCTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGTTTTGTATAGAGTGTAAG
CCATGTGT'TTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAAATGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAATTGTTGA
AAGAAATAGCCAACTATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTGCTCAAGGTAAAAGAAGATATGAC
AGAAAACAATCCGGTTATGGTGGTCAAACCAACAAATTTTCCACAAGAAAGCCAAGACTACCAAAA
AAAGTTGT'TTTGAGATTGGAATGTGTGTCTGTATAAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTCGAATTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLECVVCKTKAQLPLKRCKHFEELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAAGTGT'TTGAATTTTCAAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAGAAGCACATAATTTTTTGAATGATTCACGAAAGAGTTT
CATAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTTCACGGGAAAGCAG
CAGCGCAAGTTCAATAATAAAAAATTTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAAAACCGAG
TGTGCAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCCTGATTACTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACCGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA
TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAAACGATTTCAGATAAATCAGAAACGACTCAACC
AAAACCTTGCCCGCTCAGAATCATTGCGGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTTCAAGTTGTGGCAGCAAA
TGTGCTGGAGAACAT'TGATGAGAATGAAAAATTTTCAAGAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAAAACCTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAATT
GAAGAAAACAAAATTGAATACTATTTTGTGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCCAAGAACCAGAAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTTCAAA
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAGTGAAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCACCTAGAAGATAGATTACCAATTAAAAAAGAGAAAAATGCGGTGCGAGAA
TGCAAGACATCTGAAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTTCGAAGAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT
CACATGCTTGCATGAGGCAGCATTGGAAGGTCATACACAAATTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGCAGCTGA
AAACAAACATCTTGATTGTGTAAAGTGT'TACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTTCAAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT
AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAAGAGAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAAACGGCCACAC
AGAAGCTTGTTGATATTATAGCTAGGGCTAAACCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCTTGTGTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTCACGGGAAGTTAGTGTAAATGAAATTCATGGAGAAGAAGAGTGGAAAC
CAAATTTTGTCTGGTATTCGGTCAAGGGTAGTATCTCGTGCACATCTCGTGCACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAATAAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
CCAGGAGTCTACAGGTCGAAAACCTGAAAAGACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTGTAAATTGAA
ATCACTACATAGAGAATTCATTCTGATGATCACCACACCAGTGAAGCCATTGAGATTCTTTTGC
AGAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAGAAGAACAATAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGCAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACGGAAAGAAGAAGAATTCGAGACACAAGAAGAAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAGAAGAAAGAAAT
GGGGTTGCGACAACAGTTGACATTGATCATTCGGTTGGATTGCGTTATTGCAAGTTTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA
GTATGCTGTTGATTTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATTTGTGGAAGCTCTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTACACTCAAAGCAAAAGATAACCAATTTGATGTTAGTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTTCCAAGAA
AATCGAAAAGTTTATTCTCTCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKTSFTDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKLDNKSEPNSEVNLKDNNDSSKATAGCALGPDKNKGKNDSDKSETTQPKLARSEFADT
SLLSPVNESDITDFNFELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEDEGKLLR
EQTADVCRHKLKKTCLNTIFSSDEEEEEIQEPDFKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
VKNKEVKEVGEKERNHQLDRPLIKKEKMRSENAKTSSENGVSSKSESKISKSKLPYKVRDSSGR
SLLQRAKCKGNFADVQDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKIYKYAAENSKEKTAIEYFVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
DGLNALEIAQHSPHFDSEVSVIMKFMEKKSCTKILSGIPSRVVSRASTRAPSVPVSSDEDDVVEE
KEITAHATENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMLKSEKEKEQKRKEEEELRAQEEKRIAKAQEEQERLAREAE
EKSKELEEKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVVIDDKKYAVDLQVSLIT
STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDRSSITNGQKQFQNLHLFVE
VDLAEFLKEFPVHSAKDNQIDVSLESLSGSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGATTTGCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTGT
TCGTGTCTCGGTCATTGAGGTTGGGTAAATGTTTTCTTTTGAGAATTGTGAGCATGCAATGTCG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

TAGTTTTAAACCTAAAAAACAATTTTGTGCAGTCGTGCACCATTCGTTCTATTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGGAAATC
CCCTTTTGTATTACTACAATAGATTAAAGTAACATAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAAATACAACGTGTGAAAAATCCATTTTGTGCTGTAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACGTGCTGTAAGAGAAAAGTGTGGTCACACCAATCAATTGAGACCAGAAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPSLKALASKYNCEKSICRKYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAATTCACCTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTGTTGTTCCCTACCTCTTGGCATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAGATTATTTTACCACCGTTTTCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATTTGTTGAGTTTTCGGTACATCATAGCTATCTTTGTACAATTGATTTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTTTTGTGGTTTGTGGAAACAAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTTTTTTTTTTTTACCAGCATTTTGTCTTGTCTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTCCATACATAACTTCTGACGCGTGCCTATATCTGCTAACATACTC
GGCAACAACAAAGAAAGAGAATTTGAACATAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAACGTCGTTACAGTCACCACTGGAAG
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAGCAAGAAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTTCTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAAATAGATTTTCAAGTAAAGAGGTTTGAGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCAGAGAGATACCTTGCCCAAC
TGCAAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCCTTAAAAATTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACATATGCTGAACCCAGTATTGTAATTGGTGTCTTGTGCTT
TTGTGGTGCAGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCTGTAGACTTGATGCTTTTGTGATAAGGCTTTTCAGAAAAACGGGAAAATCC
AACCAGGTGATTTATTATTCATTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCATTTTCACTGCTGGGTTCAATTTGAAAGTAGAAAAACCAATGTGTCAAGTATTTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTTCGAAGTTTACTAGAAAGCTAGATAATAGCAGATTGCAAAAGG
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAAGTCTAGTACAA
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
ATAAAAAATGGGCTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG
GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTTCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAACCAACAGATAAACTTGCAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTACATATTTGGGTTTGATCCAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTTCGGTTACAGAATCTTGTAGGAAAGCAAACACACGCTACACTAGTAGATAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHKEDAHKIDFSKRREFE
QLDKYTFTPKDVDDLEPI SKLYLRRRYLAQSQIADI I AETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLKVGNFNMNSVDLMLFDKAFQKNGKI QPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFSSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLVSVETSGHKSLSSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTSRRLLQNLVGKQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDDSKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTTGGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTTGAGTAGA
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAATGAGAAAACCAT
TTATGCAAGTCGTGTAAGTATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTTCAATGTAACTGATGGTTAAGGGATTATAAATCAAAGTGTAGTGTCTT
TTGTTTCTTAAAAACCCATCGTGGTGGTAACGTGAGGAGACCGGACATCAAATGGAATTCACACA
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TTGTTGAGGTTACAGACAAACTTCCTACAAAGCCTCCGTGCAGGGTGTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACCTTGGCAAATCGAACGTAGCAGTTTTTTTCGTCTGTTGTTGTTGTAATGCAAGTATG
CTGCTTATGCCAGCCAGTTTTTTTGGAGTATCGTGCAGTGTGGTGTTCCTGAAAGTTCGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTGTATTATAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA
AGCAATTACCAACTTTGATAAAGTTAAGGGGTCATTTGTTCCGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGAAAATCATAAGGAGATACCAGTGTGGCAATTGAACTAAACAAG
CGGCCACGTTTTACGAGGCGGTCAAAGAAGGTTAAAGTTGTTTCAATTTACAAAAGTGCAAACTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCTACAG
TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTTCGGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)
MKEPSITTTTFFVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSVTVLPESKPTVIEKLKSLGADVIIHGKHWEADNYLTDFVIKNL
DKTVYPVYCHPFDDPLLWEHGSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVHLQKVQTLATSLAPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFHYMVEPACGASVASVMHRQDLLNKFGTLLSPDDIIIVVICGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)
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GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTGCTTTGTATAATTTGCGACA
TTTGTGTTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTTATGGTTGTAACATATTTCTAGTATATTCTACGTAATAGGTGAGGTCTT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTTGATTTTGTGATTTTGAATTTCTTTCT
TTTTTTTGTCAATTTATTTATTAACATTTCTCTTGAATACTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAATCTTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCATTTTGGTTTCCACGAAGCAGC
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCACTTATTCCTGTGTTGGTGTATGAAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
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CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
TAGACAAAGGCGACCAAGAAAAACAAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT
CTTTATTGTCCATTGAAGGTGGTGTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCTAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
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CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTTCAGAAAGACTTTGAAACCAAGTTG
AACAAAGTGTGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT
CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGGCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
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CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG
ACAACAAGATAGTTGGGCAAATTGCAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
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ACTCATTAGAAAACATATGCTCATGCTTGAAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAATTAATTGACG
TTGCTAACCCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCGGTGATGATGATTCAGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHFAVAAVSDDESSTDNYGTVIGIDLGTTYSCVGM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAKNQASSNVNNTVFEDIKRLIGLKYNDTQVQKEL
KHLPHYKIENKGNKPVVKVEYQGEKTFSPPEISSMVLGKMKSIADYLGKKVTHAVTVPAYFNDA
QRQATDAGTIAGLNLVRIVNEPTAAAIAYGLDKGDQEKIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDKIVRYLAKQFKKKHNIDITANSKAISKLKREAEKAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKSIDDDIVLVGGSTRIPKVQELLE
FFDGKKASKGINPDEAVAYGAAVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAATACGTTTTAACTTG
TGACCTAACCTCATTTTTCATAAAATTCCTGTATAAAATTGGTTTTCTTTGAATTGTTTGTAATCTCTT
AAGATTGTCTCGTCTTCAGTGTTCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCTATCTTCTACTAAGCCGGACAATCCCAAAGCCGCTCTCTGTTCTTTTATTCTT
CTAAGGAATGCTTTTATGTAGTTCTGACATTCTTGCCTAAAAGGAAGTACAGTATTAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTCGCTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
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TATCAATACATAGTGACATCACCTTGCCCTAACGCAGCTTATCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACCTATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISL FVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
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ATTGATTATCCATTTCAAGTAGGACTTTTTGTAAATGCTTCTTGATTTCATGATTAAATGAGACGAGT
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
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TCAAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT
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ATCAATTAAAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAACTGGTACTAGATTTTTGGAAAAAAGGTGAAGTTAAATTCATAATG
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AATACCAATCAATAAAAAACAATTTGGCATATTTAATTGCTCATGAATGGACTCATTACCTGATA
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AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTTGGAAGATATTAATTAC
AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTACAA
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GTGGAATTACTTTTATTAAGATCAAAATGTTAATGATATTGAAACTTTAAAAGAAATTTATATCAATTTA
ATAAAAAATTCATTGATGAAGATTATTATCATAAACTTTAGAAGAATTAGTTGAATTAGGAAAT
TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KGEVKFNNETQKYEIQLDGKTLRPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLSSQHLSDMKTEKAEMLELIDIKLQMLRYLDTDTCLIFATNKECDGKLRKRQEEIYRPL
INEFNEFFTIIYAHNKNLIPRQKSIELKYLDCE TDGLRGNKQDETTQLVVDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

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GAGAAACGCAAGCAACAAAAAGAACAAGGAAACACAATCATGATTAATTATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTCTTTTTTTTTTTCAATTTTACAACCAAAGATAAACTACACAACACCCAACATTA
CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCACTAATGACAGCACAATCTCCTCTC
AGAACCATTCTAAAACCTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC
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CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
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CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
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AAAATCAACGTTTTTCTGGCAGCGTGAATCCCACTACTACGAACAACAACATCAACAGC
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MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSKTGLRKHQQQHYHQSHSQMHSQSQQSPYIN
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ETIEDGDVTTTDDDDHDFDDEDIEDPEAVQYTPPTLNILKSKKVDSFNIISSKHKRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSSQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPHTSTPMAVSSLNPPSSS
TSNSTTAAITSTSPAADHEYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPPETPIKRNPLMILNTNKVPPYSSGFAEGKDVMDQHDYSHIPCQNQRFPGSVNPNT
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IELDDNIIIPETPTKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRLSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDHEHLIEKFGMK
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EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLDFLEENKHYKIDEFRIWKILIEILNGLKFIHKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGLSDAGRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTACCAGTTTTTTC
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TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTTCTG
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GAATGAAAGGTTTGGTGTCTACAAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA
GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAAAATTTCAAGCAAAAATTTTTTCCATC
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GACCATTGCCAATGGATCAGATTGAGAATGACAACAAAATCAGATACAATGCTAAAAGAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
GATTTTCATTTGCAAGGTTTATTATCCAATATATTTCTCATCTGCCATTTATTATAATAATCACCCA
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ATATTCTGAAGAAAGAAAATCTAGATGGAAAAAATTTTGTCTGAAATTTTTTTTTTCTGTTTCTG
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TGTAGACACCAAACCTTTCATTCATTAATAAGTGTGAGTGAGTGAGAGAGAGCGAAAGAATTACAA
AAATACAGGGAAAAAATTTTTTCAGAAAGATTTATAATATGCAGGTCATCAGTTGTAACCTAGTGT
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CTTTTTCACGGTTTCTTTTATCAACAGACAATTCACCATGACTAGAACCTCCGTCTTAGCTGATG
CTTTAAACGCCATCAACAATGCTGAAAAAACTGGTAAAGACAAGTCTTAATCAGACCATCCTCCA
AAGTCATCATATAAATCTTGAAGTGTGATGCAAAAACACGGTTACATTGGTGAATTCGAATACATTG
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AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGGTAAAATCTTAGGTTTCGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGEFYIDHRSGKIVVQLN
GRLNKCQVQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)
CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA
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CTTATCCTTTCTGTGAATTTCTTGATCTCTGTTTGAATCAACAACGCTTTGTTTCTCTTTCTGCC
TCCCTCTGCCACCCCCAGTTTATTTGTTTGCTTGTCGACGTGCTGCCAAAAAAAAAAATTGAGTTC
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YJL197W_homolog 1372aa (SEQ ID NO 390)

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PISDIIRDITDDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI
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YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)

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YJL198W_homolog 896aa (SEQ ID NO 392)

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ELKSFIELNRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
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CLAVLVAAAMLWASEALPLYTTALLIPLLVTCKVCKTPGTDPMDATKASQYIFGTMWNSTIMIL
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FFGTGLLKVDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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YJR049C_homolog 592aa (SEQ ID NO 394)

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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPIVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWLLAREVLRRLRGIIPDRTTESWSVM
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YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
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YLR088W_homolog 444aa (SEQ ID NO 398)
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DLLNTANVMITYHEQIPCAMQGMSTRVINYSTRLQTLFRGILKLTGLVLTDEVHGCFAFSGWQIQAF
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ALLAVALLLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
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YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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CCTTTGTTCTCATAGTTAATCCGACTAAAGAAGTGTTTTTTTTTCTTTTCTTTTCTGCTATATC
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TGACGCTGACGATTAATAATGTGAATTTCTTTTCTTTTGGTTGTAGTAATTTGCTTTTGT
TGTCTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACACATACCACTGTCGTGCACGTGACC
AACAACAATGCGGTGTTAATCGATAACCAAAAGATTATAAATAGGGGGTGAAGGTCGCCACTGTT
TGAAATGAATCAACACAGTTTTTTTTCTTCTTCTGCTTTTTCTTTCTATTTTACATTACAAATCTGA
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAATTTTCGTTAAACTTTGACTG
GTAAACCATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG
ACAAAGAAGGTATTCCACCAGACCAACAAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA
GAACCTTGCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTAAAGATTGAGAGGTG
GTATGCAAAATCTTTGTTAAACTTTAACTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
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CTATCACTTTGGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGATTGATTTTGTCTGGTAAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACATCCAAAAAGAATCTACCTTGCACCTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRRLRGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRRLRGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
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GCACACAACAACTAGTTTACAAAGTAAAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTCTCATCAAACTT
GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
ACAAAAAATAAAGGAACCTTTAAACAAGAGTAATCCCCATTAAAACTTGATCAACACTTTT
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CATCGATTTCAAAGAGGTGGCAAACATTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG
AAAAATTCATCAAAAACACTACGATTTACCTTACCTTTCAACTCTGAAGATGGGCCATGTCAAGTAA
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA
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AATACATTGGATTTGAAATTATGAATGCTGCAAGAAATACAATAGGAACCTTGGGTAAACAATA
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GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAAACGGAACCAAAATTTCCGTCCATTCCCAT
TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTAAAGATGTCTGCTAAGACGGCGTTGG
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCGTATCCTAGAACTGAACTGACAGGTTTG
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CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC
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TGACTTTAAATGGGGAGATGAATTTTCAACCGCAAGTGGATTAATGGTGCATGAAAAAATTATT
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CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA
ACAAAATAGAGACTAGGCACTATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCTTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGA AAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTTCGCGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGTGTTGTTCTCATCAGATAC
TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAATAGCAGTAACAACAACAACAATA
ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKKNYDFTFTFNSDGPQVMTTSVAGHITGLD
FGSAFSWGNVCVPGRLFEADIKTIITKKSİYENIAEEARNADKLMIWTD DCDREGEYIGFEIMNAARK
YNRNLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEIDL RVGTSFTRLLTDQLRQK
GII EKNELASYGTCQFP TLGFVVD RYKRVKSF TPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS
YPRTE TDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVY EYVVRRIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK
QLPKFTEGEQVKLSSGILKD GKTSPPNHMTPEPELIALMDANGIGTDATIAEHINKIETRHYINKLK
KGKNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLESLIEDIATGSRPKVDVLNTTIGVYVD
AYSVC SHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTA ACTAAATTAGAGGTTACATTAATAACA ACTTAAC
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ATTGCCTTATATACAGCTTGTA AAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAA AAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGCAACAAC TACAACAAAAA AACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACAGATAAGATTATCAGTTTCTCTCGGTTGACCTTAATCTGTTTTGTATAGACTTTAT
TTTTTTTGT TTTTGACCACACCCACTTTTTTAATATCACAGATATTTAACTGATTATAGAAAACA
CAACAATAACCCAAATACGTTAACC ACTTTTATTACATATGATAGACAATATAATCAATAATTTGC
AAATCATACTACAGCAAATGATGATAATTTTACATCCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
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CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGACATGCTGGATTAGATGCAGTTGTGTTTT
TGGAATTTT TAAATGTGCATTGCAATTAATAAGCATATGTTTAGTATTTGCCATTATATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGAGCTGGAATTC
TGGTGGCAAAGTAA AATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAA AATTCAGTCACCGATAGAACGGTAA AATATCTGGGATACCAG
GATCAGTTTACAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAA AATCTAAACAACTATTCAAAGAAGGAGAAGAAATTC
GAA AATTAGAGGAAAGTTGGGTTGAATATTTTGAAAAAATGGGATAACCAATAAGAGCGATTGTA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAA AATTCGAACCTGACACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATCTTCTGACACTTTGAATCGCTTGTGTAATGATGAACCTGAGAACAAGAC
CAAGTCTTCGGAAGGTTGGTTCCGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA
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AAGTCAATCATCTTATCACC AACTTGGCCCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCAT
TAAGTACAGACAAGACAGAAATACAAAGATCCTTGCTGTCACGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTTAAACACTAAAGCATTTCATAAATATGGC
CATCATTTGGGGAAGCTATTGAATCGCATAAATGGGCGGAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCCGTTTTTTTATGTATGGATTCTGAAAAGCAAG
GTTATTTATCTCATAGTGAAGAGTTGTCATCGGTATCCAAGAACTTTTCTATATATTTGTGA
ACTTATTTTGGTTTTTCACA ACTTTTGGTACCGCTCTTTTGTGATACGACCAAAATGCATTGT
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GGTGAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCAAGATATTAA
CTGCAGGGTACTATATTTTATTATTGGTTATTTGTGAGCAAATACCAATTGCTTTATGCTTGTG
TTCTCTCTCCACACTCAACGGGCAAAGTTTGGCCAATAATTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTGCCGTTTTTGTGACTTTTACTTTTGGTGGAGTTTCATAAACAATATATTCCTTGT

CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACGTGTACGGAAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIQIILQQNDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRNLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTYVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSVLIVKEWQNLNKLFRRRRIVRKLEESWVEYFEKNGITNKS DLI SLHPQVGESYRF
SNRYTDDAESPDWGSQNSNSAQASIIDQDSESEVGDSDDLNRLLNDESRTPSLRKGFGLFGP
KVDSINYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPISLGAIESHKWA
ETLITGLLPYTLFTILNIVIPFFYVWVISEKQGYLSHSDEELSSVSKNFFYIFVNLFVFTTFTGTAS
FVDTTKIAFDLARSRLRDL SMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGQLPQPILIFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPHSTGKVPWI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTTGGAGAACCTGTGTGTGTGTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTTGAAGGAAATCTTTCTTAAAAGCATCTAGTGACACATAGTCTCTCTCT
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GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGTATATT
TTTCTTTTGTCAATCCATCTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTTCATTCCTTTCTTGTTTGTCTGT
ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGCAACTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAAATTCATTACTTA
TTAATGTTGACCAACTGGTGCAGCAAGCCAAAAGACATATTCAACAGATTAATTAATCTCGAAGAGT
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ATAAAGCTCAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT
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TTACACCAACTGAGTTTGCGGAAATTTGTTGTCAGTGATTTAGATTTACCATTTCAGTATGGCTGCAC
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GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTGTGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACTTGCATCTAGTAAAAGGTA
TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAAATGACCGTTGGG
AACCTTTGGTTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSF PKRLANDSDNSLLINVAPTGRQAKRHIQQIN YSEEF GDDLDFDEFPS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSDDLDPFSMAAQIAD SINQIIEEYSYASN LQLENKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNHLVKGIMFEQGIRIFTENS VQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRDY
DDHSRRRQAGKRRYDELEGA W

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
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TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAAATTTCTTTGAAAAAATTCACA
TCACGCTTTAACCCTTCAACCTATAACAACCTCCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAAAATTCAGGGTCAGAGGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNANVGKKFKQTKFKVGRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCC CGGGGAGCTAATTATACCCTCATT
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CGTTTTATATTTTTTTAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
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AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTAAGTTTAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTTGACTGAAGTACTACACCAAGAAAGGTA
TAATGATTTCCGATTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTTCAAACCTGTTGAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCCTCAATATATTCCTTCCTTATCTTACTTTTCCT
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TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
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TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATCTGTATTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCGAAT
CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKS LPIRQNDV LVVVRGSKKGS
EGKVN SVYRLKFAIQVDKLQKEKSN GASVPINIHPSKV VITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTGAAATCTTCCCTCTTGGAACGACCAAGAGTTGGATTGCGGTGCCCTTGACTAGCAC
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TGTACTGAACGTCTTCATCTTCATGCTTTGCAAAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATTTGCTTCCCTCAATCTGAAACATATTCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAACTAATAACAATCTTCAACACCCGATCTAGAGTTTGATTGATTAAACCATT
GCGTAATTGGATCGACATATCTTGTTATTTTCTATGATTAAATCTTTCTTTTTTCTTTCTTTTTCAC

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAAACAAC TTGT
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CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTGTACGACTCAT
TAGACAATAGATTAAGCATAGTCAAATTGTTTCTCTGTTGCTGGTGAGCAGTGTAACCGTTTCGT
ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCATCTTGCCTGGCC
ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRFFPSYFFSLSLFFQSHCSSVKGWLFC AEPCGSVNARHRV
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RPLGLSKPVLLNHKLSDTYSLSNIEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQRSLYDSLNRSLIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPPASRYENYFILPGHIMS AEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMMKVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

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GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTGCTCTGAATGTCGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGATTGCTGGTGCGCAA
AAAGATTATGTGTTATTTTATGTGCGTTGTTTATCTGCACACTAAAATTGAGCAGTGTAACACACA
CATATTGGGCTGTATTTTTATTCTTGTTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCCATA
CTACTGAAAATTTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTCTTTTACGTT
TTTCACTTGTTCATATAATCACCAACTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTGCTTGACCCATTCCACAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAACTTTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTA AAAACTTGTGTA
CCAACCTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACTGTTAAACTTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAAGACAACCAAAACCAATCAAGAAAACTACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAACGTACTTTAGCTCAATTAAC TT
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCAATTTCCCATTAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCAATTATGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEDSYRKIKLRVDEVQGNLLTNFHGLDFTSKLRSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLEVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFFLPQNVHIRKVKLKQPKFDLGSLLALHGEGSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTTCAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
TAATTCATGACCTCGAGTCATATTTCCACGTTTTTAAGTATGAGTGTGTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAATAGTAATAAAAAAAAAAACCTTCTTTGCTTTTTCGAGAATTTGTAAC
ACATTGTTTCTTTCTTCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTTCACAACGATTGCTATATGACCCCCCCCCCTAAGCATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATATACACTATTTGTGACGTTAATTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAGAACATTTAATATGTATTTCCCAATCATTTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATATGGTTTGTATCAATGGACAAATGATGATTTAAAC
AATTTTAAAAGAAGCTAAAGTTGCATTCATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT
TGAATCCTCCAGATGATTCATTAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTCAATTAAAGAATGGATTTTGAAGTTGGCCAGTAACCAGTTGCAAACCTTTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAAGAATTTAGTTATCAAGCCACTCATTTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTTCATTGGATTTATTTGATAAAACCATTTTGTGATAAAAAGGTCAAA
TTGAAGATGAATTTTCCAACTTGGTCATATTTCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAGGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAAATGATA
CATTTCTTGTGTTGTTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKQKRVAFNDALNPGLISLANEEAKKLEKGYK
KVTEELNNLNPPDDSLNDYLNFDYLFQKRKENYSIKWIFESWPVTSLOFLTONNIQYSKDTK
DDLINKVKDQFDSISKKNHGSSFPYGNWLYESWSENLDKDWLKSQYIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDLDFDKTIFDKKGQIEDEFFQTSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATCTGCATAAAGATTAAAGTGAAA
AACAAATTTCCGAAAAAAGAAGAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACCTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACCTCAGAAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTTCTTGCCTTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTTGATTACACAGAATTTTGTTCACAGATCATAACTCCCCTTGTAAATACAA
CTTTCACTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGGAAATGCTCAACATTTT
GTGCTAGTGAAAACCTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAAACCTTCAGGATTAGGTAAGATTTCAATTACCTGACAAATCATCAATTGATAATTCATTG
AAACCGAAGAAGTTCAAACCTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGAAGGCTATTTACCTGGAAAATTGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGCAATGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTAGTGGTATGTCATG
CTTCAATTGTCAGTACATTTATCAAGAGAATATTTGAATTTCTGAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAAATTGAGTGAAATTTTACCATTGAGAGAGTTCATTCAACTGG
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTGCAATCAGTCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTTGTTTGTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACATGATAATCACAATTTGAAATTTAGAAGAA
TTGAAATTTGTGCTTGTATTAATACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTCAG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTGTGTAGTCCATTACCTCAGA
AAAAACCTGACCAAACCAACACCCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATGCCCCACAAAAACCTGAAGATCGAAGCTTTTATTGAAGACTTCA
GATTATCCCTTTGATGAAGTTTGGCAAGCATTAAGATTTGTTTAACTAGTTATCAAAGATTTCCAG
CCGTATTGAGTAGATTACATTGGTTCAATTGAATGAATGGTGGAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKSIFYFRYFKVNLQKQCRFVNAQHFCVSENCVEILEDNFWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGNGQSFVWKAIYSENCFPN
TNPMSVTNDADNGGEQCIENLFFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIFYFNALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLNNDVESVEVYDRLLDDIIP
SLEANVVFNSTNLFDNSNLRDEFRRSRFRNISAIMDCVGCDCRCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKQPDQNTNPKNQKQKQPDQETDKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAACAAGT
AACAAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTTCCCGCGTCTGTGTGGCAGGACAAATTG
AGTCGACCAGTACGTTTAAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTTCCACTT
ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTTCGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCCAACAACCTAGATTTTCCGAATGCCAAACGACGAGGACGACACAACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT
TTCGATAATACTACCACCACACAGCTCATTCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATATCCATATGCAAATG
GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTTGTTACATCCAATATTTATGCTGATGGAACCGTTTGTATTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATAATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLEQYQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTCCCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTTAAACAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTTTAATTTTTTTGATCAAAAGTACACTCATCAG
TCTATTGTCTGATGTTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTGA

TTGTAAATTACAATTTTTCTATTGGTTAAATGATAATTGTTAACAAGTCTTTTTTTTTCCCGGGA
TTGAATCCGGAACTACCATTAATTCACCTCATCTACTCACTCACCTTACACCCCTCACTCACTCAA
ACAATTATATCAACCCAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTGGATCATGTCATCATTTCCATAGAA
TCACTGGTGTGTGCTATGGCCGGTGCTTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT
TAAATATTCATTTGATACTACTACTTTAGTATCTGCATTACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAAGCTGGGTATGCTGTTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MTSRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTTAATAAT
TATTTAATCAAACCTTGGTTGTAACCTATGATTATGGTAGTGATCTAAGAACACAACTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTCTTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTCTACACTACTAGTAAAAAATTTTCTTCGCTCACTATTACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTCTTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG
CCATATCACGTTTCAAGAAATATTTAAACAAAAATGAAGAATAAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTCTGTTGTTGCTAAGAAAGACTTCAACCAACCAAGCAGATGAAAT
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATCTTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAAGCAATAGGTCAT
TTATTGCTGTAATCAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTGTTA
TTAAACAATATATTTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCCTTTGCATATT
TTTTTTTTTTCTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAAGTAGTCG
ATATGTCTAGCACTGGAAACATGAATGAAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAAATTCAACCAAAACCGATTTTTTTGCTGCACGATTGGCTAGTGGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATACATAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACTTCCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTGAG
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAAGTAGTAGTGTGCCCCACTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTGCA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA
GAAATTACAAAACCTCATCCACTTCTCTCAAAATTAAGATCAACTACATCAAAAAC'TTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTGATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAAGAATCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAACAACAGTGCATCAATATTAATTTCTCCTTTGACTGCTAATAATAATAATAAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACACATTGCTAATAATAGAG
CATTTCCATTTTCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG
AATCACAATCAATGGACCAATTTTGTATTGTCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAAACAACAACAATAACCCCAAAAGATTTGGCGACAGTCATTTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTTGT'TTTGGCCACAACAAAAGATTTAACTGATGTAGGTA
TCACATCCATTGAGAACCCCATTTAGTAAAGATGAGTTAGTTTTCAATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCGGTTGACATCAATGAAGTAGAGTTGGATTATTTTGAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTCAAAAGGGAGGAATCCGATTATTTATATCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAATAAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACTCCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAAACTGGGTATATTGATCTTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNNDASNNNNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVPRQQQFKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKL
STTSKLFDKKGSQPRRYSTIPDDIDIEDFDELIYDNTARFPANESTSLLNQNRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTONGNNSDHNINSPLTANNNNNNVNHNHGDNKKSN
NNNNIANNRAFPFPYQDQQHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPWFVSVDINEVELDLFARSGYLPDTONSKI SNMGGSQKVETVKLGITILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTGYIDPTLFVIPQGENNIS

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;

CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTTACCAACCAAAACCTCTGATATCAATGATTCGAAAAGATTCAATTCA
ACCCCGTTAGCTGTTTGAAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAATAAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAAACTTGTGTTGTTAGATGAGCTCAAATATGTTTGGTGGAACAATTGTGTAGTAGTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAAATACCATCGCAAAAATCCTAACAAAAAATAAAT

TAATAAAGAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTTAACAGAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAATAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTTACGATGAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCTGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTCAGATT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCCTCATGGCCCAACTGCGATTTTCACGTTACATAATGTCA
AACTAAGACACGATTTGCCAAACTTGGGAAACGCTCAGAGTCCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAAGCGTGTGGTTAAATATTTGCAACATTTGTTTCCCTCCAGGTGTCA
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATG
TTTACGTCAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTA

YNL075W_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKLSKELAEDEKLQDRFIYDESEIEI
DDEYSRLSGISDPKVVITTSRDPVSKLLQFSKEIKLMFPNSLKLNRGNYIISDLVSTCNRVQVSDM
ILLHEHRGVPSLTVSHFPHGPTAIFTLHNVKLRHDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPVPGVKDSSRVITFVNDDYISVRHHVYVKTGDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGAGGAAGGGACCCGGAATTCCTAGGAACAGGA
AAAATAAAAACGAATAAAACAAAAACCCCCAATCGGCATGCATCGGAATTCCTTCAGCCCAATTAC
TTTATTTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTTAGCCCTTTATA
TGCAGTCTATTTTTATTTTTCTCTTTTTTTTTTGGCTGTTGGTAAACTTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATATCTTTACAGGGGAGTTCTTTTCTTTTGGAAATAGTCAACC
AACAGCAATAGCCAAGGATCAAGCTTCATCTTAATCATGTCTCTAAGATCTTATCAGACAAACC
CAACTGAATTAGAATTAAGAGTTGCTCAAGCTTTCGTTGATTGGAATCTCAAGCTGATTTAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAGAAATTGATGTTAATGGAGGTAAAAAGCTT
TAGCTGTTTTCTGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACCTAGATTAACTAGAG
AATTAGAAAAAAATTTCCAGATAGACATGTTGTCTTTTTAGCTGAAAAGAAGATCTTACCAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCATGATA
AAATTTTGGAAGATTTAGTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAAATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELEKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVVFLEERRILPKPARKARKQQRPRSRSLTAVHDKILEDLVFPTI
GKRVRYLVGGNKIQKVLDDSKDSTAVDYKLDLSFQQLYSKLTGKQVVFEPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
501..1253 (SEQ ID NO 431)

TGTTTTTGTTTTTGCAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTTTTTACTCTCC
CGTAGTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGTGTTAATCAAATTTGCAATAAATA
AAAAAAAACCAAGCCGACAAAGTTTCCCTAAAATGACTTATTTGTGTAACGCATTAC
GTGATCATAATTTTTTTTAAATTCAAAACTGAACCAATTCCTGCATATTGAGGTTGAAAAAAA
AGAAAAAGAAAATTTTTTCAATCTTGTGTTGAGGAGAGAGAGGTGAAAAATTTTTCTCTCTCTCTT

CTTTCTTTTCATTCTCATATACCATAAACTTAAACAACTTCTTTTACTTTTTCTTTCTTTCTTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
AACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAAC'TTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGT'TTTATGATTCATTCTGGTCAAC
CAACTAGAGATTTTCATTGATATTGCCATTAGACATGTTTAAATGAGACAAGGTGTTTGGGTATCA
AAGTTAAATTTAGAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATCTGTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGCTGTTAAATCTTATAAAACAAA
CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEEQGR
IHELTSLVIRKFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRPFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMHSGQPTRDFIDIAIRHVLMRQGVLGIKVKIMKDPANRF
GPRALPDVAKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAAATCACATCTTTCGGCATATATCAAACCATTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTGCCAATTCATATGCTATTTGAGCTCCAATACCAGTGGTCCCACAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCACGCTATTGGTGGCACCATGGAAATAATACTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCACCTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCACAAATTGGTTGCCTTTTTATTCT
TCTTGTCTTTTTTTTTTTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAAAAAAATTTTG
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATTCATGGATATG
TTACATCAATCCATTCTTCCAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAGGAGAAAGAATTTTCACTGCTGTTCCTAACAAGGCATTAATCA
ATGTATATTCATGGGGAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA
AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTGACAGACGCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTTAATTAAGTGGAGGAGAGGATGCCAGATGTCTGTATGGAAT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAAATTAT
ATACAACCTTCAGAAGACAGCAGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTTAACCACAT
TTATTTTACCCAGTTCCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTAAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAATTTAAAGAGACATTTGTTG
CACATCAACAAAAAGACGAAAACAGGAGAGGATAAGCCTGTTGTTGTTACGAAATTTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTTCTGAAGGCAGAGTGTTTGTGTCTGACATTGTAACGA
AACAAGTTGTGAAATCATTACACCTTGTAACCTCCAATAGCTTATATTGCTGTTGAAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTCTGAAGAACATCAGATATTCTTGGACA
TTCTCTGGTAAAAACCACGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAGAACATGCCAAATTTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNRYVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGSSCGTFLITGG
EDARCLVWNLAELISIDYKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTFFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQQKTKTGDDKPVVVKLTISFDGTSIISGDSEGRVFSVDIVTKQVVKSFPCNSP
IAYIAVETIPDDFVNMLATST'TNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTAT'INATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSLEERLQRVSQAYTEL RNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTTGGCCGGGAACGAAA
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGCTTCATCAGTTATAGCATTTCAATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTAT'TCTGGCCTATAGCGTTT'TAGGAAATTGCGGTATTTTCTGTCT
GTTTTTCTTTTATCTATTTTTCGCACGACTTGGGGTGGT'TTGTTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATTGACTTTTTTTTTTACTTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTTCTCATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTCGTTT'TGACAAAACCAGTAGATCTAAAAAGC
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAACCTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACTCTACCACCTCTAGTGGTAACAATGGTGTGCGCCACTGGTGTGCTAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGTGCTTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFAISSLAAAKGGEKDHGKASTVTKYVTE'THRYGRFDKTSRSKKPKETGTHRYGKFN
KTRPRVTTTTLVKESDLPKKRDAVVARD SKNASSNSTTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCCTTTTGTTTTTTTTTTTTTGGGTGGTGTGCTGCTGCTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTTCTACTTGTTCCTTTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGAAAAATTAAGCTTGAAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTTCAAGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACAGCTCAGCATTTATTTTTCGTTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTCT
TCTCTCTCAACTCAATTTCAATTTTCCCAAACCAAAATTTCTTTCTTTCTTTCTTTCTTTATTT
TTTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTTATTTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCGCCGGTGGTGTGCTGGTGGTTATGGTGGTGCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACAGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC
CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGTGLGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDRDRDRR

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCAGATAGCTAACGGTTTTGCGATTACGAATTTTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTATTCTTAGTACAATGGAAAAAAAAAAAAAGAAGCAAAACAAAA
AAACGAGAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTCTCTGATTGTGTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTGAGTAATTTTGACGCAGCTTGTCT
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGAAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTACGATCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTTCCTCAAACTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAAATTTATTTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNNSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHHRKTVSQG
DLSNFDAAACSEIESFKPHESDVERLHLALDLEELSHDIEFGVKLTSKAIQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTNFDKSYVDNLFQELANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVEESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTTCCTTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAATACTATCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTCTACCAAAAAACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTAACCTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATACCATTAATTTCAATAATCAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAAACAACACCGATTCTATTTACCAACTAACACG
ACAGAAAGGGGTTGTACTATTTGTAAACACATCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTTCCTTACACTAGTCATTTACCTGATTATGTTTTCATTGTTCTTCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCCTGGTATAGTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTCACAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAACTTAGGAGGTATA
GAAACTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTTCGGTATTTACTTCATACCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTTCACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIVYTLMLGVLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRACANDV
VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFLSLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFMFTNTLGAALWAVDIEQQE
KAVTENVAATTTATDTNSVNQQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:

948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCTATAAATTTCAAAGTCAAAGACAGATCTTAAGGTCTAATTAA
TAACTCTCTATGGCCTTCTGTGTCAAATTTGTGTCGTTTGATAACAAGTTTGGAAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAAAA
AAAGAAAGAATTTTTTTTTTCTTCCATTTTCAAATTTGAGAGATCGAAATAATTTCTTGAATTTA
TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAGGCGATTGAAGCATTCCTAAAGCAATTG
AAGCATCACCTGAACCAACCATGTTCTTTATTTCAAATCGTTCTGGATCTTATGCCTCTTTAAAG
ATTTTAACAACGCATTAAAGATGCTCAAGAAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGGTATGACAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCCTTAAACTAATCCACAATTTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGGCTTTAATGGGTATTGACATGGATTTACCAATATGGGATTCATGCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACTGGAACCAAAATCAGTACCAGAAATCTAAACCAGAAC
CAAAAGCAGAACAAAGGAAGAAGAATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTTCTAATCGTGCTGCTGCATTGGCAAAATTTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTTCATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTADEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLVSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEEFLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGDDKDLGF
GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTFAALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEESTSAKDEDTPMTDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNIIYLKKDELPEAVKNFEKSLTEHRTPDVLNKLRLSTQREIKTRELNAYIDP
EKAEEARLQGKEYFTKGDWPNNAVKEYTEMIKRAPEDARGYSNRAAALAKLLSPDAIQDCNKAIEK
DPNFIRAYIRKANALAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMKNKATYQRFQAIEGETP
EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKNMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGGACTATACACCACTGAAAAAAAAAAAAAAAAATTTTTGTAAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAAGGGATCAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCTACCCCCCTTGTCAACTTGTCATAAATTTTATTGCTCGTCCTTTAAAAGAAATGAATAA
AAAGATTTACTTAACCTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAACGAATATCAAGTTA
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAAGATGAGAATTTTTGTCTC
CAAACACCGTTTGTGGCAAATCAAGATATTGCTATTTCTTGCAAAAATTGCATAAAGTTAAAAAAG
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAGTTGTTGAATTAGAAAAACTGATGATGTTAAAAGACAATACGTTAAAC
AATTTTGGACTAAAGATTTGAAATTTCCATTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHNMKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVVKQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAAACAACAATA
TTAACATACCTTTGTGACAAAGCAATTATATTGAAGTTTTTTTGATACAAGTGTTGTTTTTTTGTG
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YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEIVVEEVVVEEQSGAITIEDALKVVLRSLVHDGLARGLREASKALSKREAQLCVLCDSV
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RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)

AAAATTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTCTGTTTGAAATTTATCGTCCT
CATTATCGTTGTCATTTTCATTGTCAATATTACGGTTACGATTTTGTTCCTTTGAAG
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ACAAACTTTTTGATTGATTGCAACTGAACAAAAAATACGACAGACACACACACACACAC
ACACAATTTTCAGCTCCTTCCAAGTCGTGTTTTTTTGGGAAGAAAAAACAACCTTGGCCCTAAA
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AAACAAAAAACCCCTAACTTTTATTATAGTTTGTGTTGATGTTATTTGTTTTATACTAACTAAAA
TCTGTTTTTTTTTTTTTTTCAAAGGCCGATTCTATATTTAATGATCTAATCAACAATATCATTAAC
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ATAATGAAATTGAAAATTCAACAATTCAAGATAAATCAAAATTAACAATTAGAACTTCAAGGT
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GTTTAGAACGGAAACGGAAATGA

YPL047W_homolog 126aa (SEQ ID NO 450)

MLFCFILTKICFFFFSKADSIFNDLINNIQHTLTSLTNIKDHSSLLNSSNSNTNSNTNGTIAN
GGNGTTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS:
1250..5341 (SEQ ID NO 451)

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TTTTCTCCTTATGGAAACATTAGTACTAGTAGTGGTGGTAGTAGTTGCTGTTGTTTGCACCTTGC
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GGGAAGAAAGAAACAACAAAAGGGGAATTTGAATATACGTCAATCTTTAATCCTACTACCACGGG
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TTCTCAATGTGTTGGTGTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTTCAT
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GAACATTGAAGAACTTCTGACTTGATCAAGTCATTAATTAATGTTAAAAACATTACGATTTTTAGA
TTTAAGTTCCATACCTAATATCTTCCCGAAAAATAATTACCCATTTTGGACAAATACTTTGCCAGATA
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GGGGTGTTTACTGAAAATGCCCAATTAGTTTCATGTCTCGTTATTGGGTAATAGAATTTGTCAAC
TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA
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CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
GGATATCAAAATGCAAAGAATTATATCCGATTCAGTATTGGAAGAACAAGATCGATTTCGTAAGGA
TATTCACAAAACCATGATACATTTTGATCTTAATGAATTAACCGCACAAAGCTATTGGGTCATTGGC
AGAGAATTTAGTTCGATTTTGTGTTATTAGATTCTGCTTTAGAAAAATTGGTTGTTATGGTTGAGGA
ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAATGAGTTGATTACTGCTGGACCAATTTT
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AAATTCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT
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YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNSPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNQDQDVLFRGKSKKLGGKMMANN
NANKDERKNSHGNINKSEKTTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSSASTVVPSSSTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSNSSSPNVSRNSKKGGLFSSLSKFR
SSSASSKQPKSHSSSTPSTTTTNGGNSAAAPKSSSHSPKFNPSLVGPVSKHNREEDLVSLNTNL
PAGSGIPIKRSFISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIEEISEVRLRRVTFVVDKLEHDPQQQIPSRPKRGNVLIPODINAPPPRLCLGISV

NEPNNKDDGKSHNHSKYSDEHIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK
EGGSVGNSTNGNDNDEDDDEVEEAVDKKLANDVSDGPLHVHEQHFEIEIESKTGEKTI SLETIY
TRCCHLREILPIPATLKQLKNKTAPLEVLKMLNPKPTLIDVLSFSDFIAITPINTVIFDNVTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQORIKPDPDTSIRGNM
NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLT
GNSQCVGVDFIAFNDLSKGQLRPFINAFNTGKVNVLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF
LDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLLGNRNL
STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL
MYDGSLLMETAEKLLVEIEKGKKEDIKMQRISDSVLERTRSIRKDIHKTIDTLFEQRNLGKLSFE
GKENLVRFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGP
ILSPHVNRKAEQSSYFPVFANNDNLTPHQVVESNDEGRDVPIDKMTGRPVILRSISQTSVHAKEQ
EIEEGELHKFGFFIQKKERQKQQQQQQQQNSHHQHQAQSIQQENQSPSPQQGYEDLPILNTLP
SGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS
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YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:

394;CDS: 501..1856 (SEQ ID NO 453)

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AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAA
TTATAATGAAGTAAACATGTAACGTGTGAATTTTATTCAAGTCAAAGGTATTGATTAATATTG
TAGAGTGTGAGCATTTAAATATGAAGGAAGACCGATAACCTAAAGTTTCTCAGGGTGTGCGAA
GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCGTTTATATCAGTTTTTTCGAAGAAAAAAGG
AAAACAAAACAAAATAACACCACAAACGAATTACACAAGCACATCCTAAACACCACTCTGTTGGAG
CACCAATCAACCTGAGAAATGCAAACTTGTAATAAAATATGGGATACAATATAGCAATGGTAACAG
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CGAATGGTTTGAAAGTGTATTATGTACCCTTTGGGTGATCTATAGAAGCTCAGTTTTCCCAACTG
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TGACAAGCTTTGCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA
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YPL175W_homolog 452aa (SEQ ID NO 454)

MGYNIAMVTDFFYPQPGGVEFHVYHLSQKLIELGHSVVIITHNYSSRNQVRVLTNGLKVYYVPLWV
IYRSSVFPTVFCFPILRNIFIRENIEIIHGHGSFSTLCHEAILHGRTMGLKTVFTDHSLFGFAEI
GSIMGNKALKFTFSDVGHVICVSHCKENTVLRGSIDPIKVSVIPNAVISKDFPKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGA
KHAEVRDVMVQGDIIYLHPSLTEAFGTVIVEAASCGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAAIDAINKIESNEIDTSKFHDAVAKMYSWNIDARRNTENVYNSLDLCLKLNLHRLQRYCYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIIKEEDESEETTFIFPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTCCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA
AATAATTGAATAATGATATAAATATAATGTTGTGAACTTGTGGAAAAATTTGACAGCCTAGTAAC
TCAAGTGTGTGTTACACTCTTGTATTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA
ACAGCAAATACTGTCGTTAATAGGAATCAGAGGCAGAAAGAAAGAGAGAGAAAAAAGGACA
CATTTACACGTACACCCTTAACCTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA
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AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTTCCATTTGTTATTTTGGGTAATAAGATTGATGT
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAACTACTGGTAAAGA
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TGGATATGGTGAAGCCTTCAATGGTTATCACAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWVQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
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VPTAVGEMELKNALGLYNTTGKDTGKLPETRPVFMVSVVMRSGYGEAFKWLSQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)
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ATTGCCACTGAACTGCTATGAAAAAGTCGAAGATGGTAACACTTTGGTTTTCAGTTGACATC
AAATCCAACAAACACCAAATCAAATCTGCTGTTAAAGAATTATACGATGTTGATGCCTTATACGTT
AACACTTTGATCAGACCTAACGGTACCAAGAAAGCTTACATCAGATTAACCTCTGACTACGATGCT
TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIIVAP
IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACCTTAGTTCTTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAAGAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGGCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT
AAATTATGAAAAACGTCAAAGGAAAATTCCTTGAAGGTGAAGGTGAAGAAGAAGATGACGAATAA

YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLEARNISYVATIFGGAFAPQGFFDVAVNKWWEHNNKAKLWKNVKGKFLEGEGEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

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CCAGCTGAAAAAGCTGTTAAACCTGAAGAAGATGATAATTATTTGATTCCTTATATTTTAGAAGCT
GAAAAAGGAAGCTTTTGAAGAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
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YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
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TNKKRTRKRKKMRRSNIEI

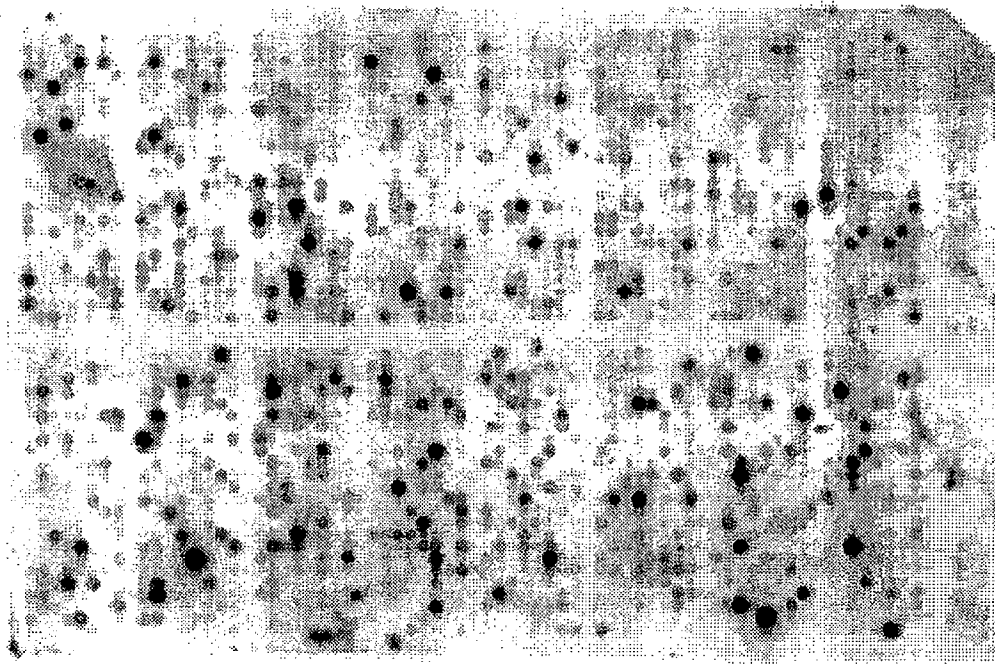
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

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TCTGATGGCCAATTGTAAGTGTCTTGGGATTATTCTGGATTTCTTGTTGTCTCTGGCAGCGTTACC
AGCTAATTCCAAAATTTTCAGCAGCTAAATATTTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
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CAT

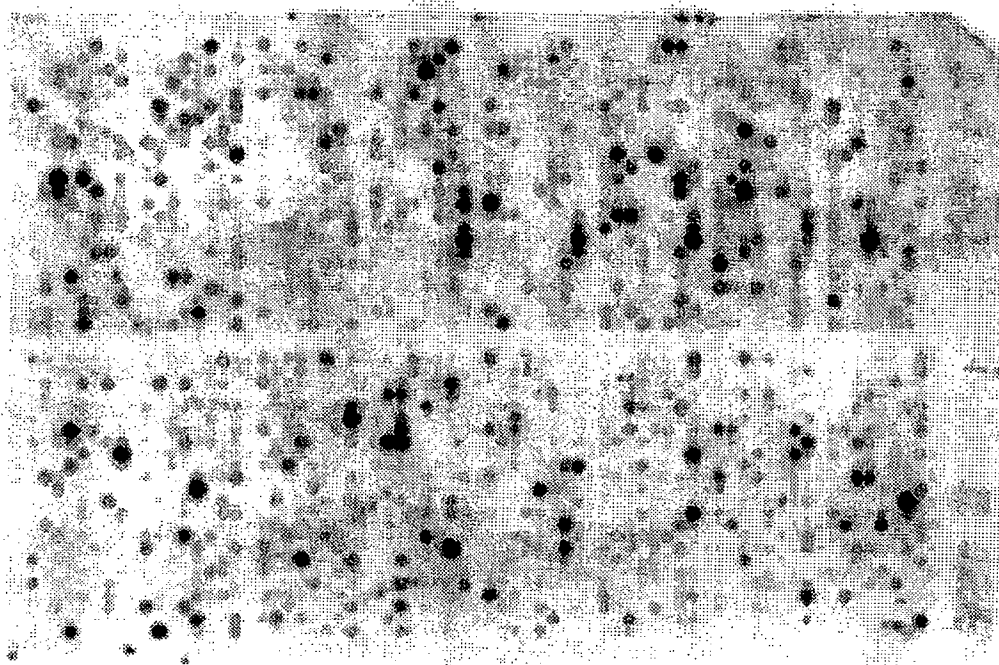
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

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AGNAARDNKKSRIPRHLQLAIRNDEELNKLGDVTIAQGGVLPNIHQNLPLPKSGKGGVKASQEL

158/161



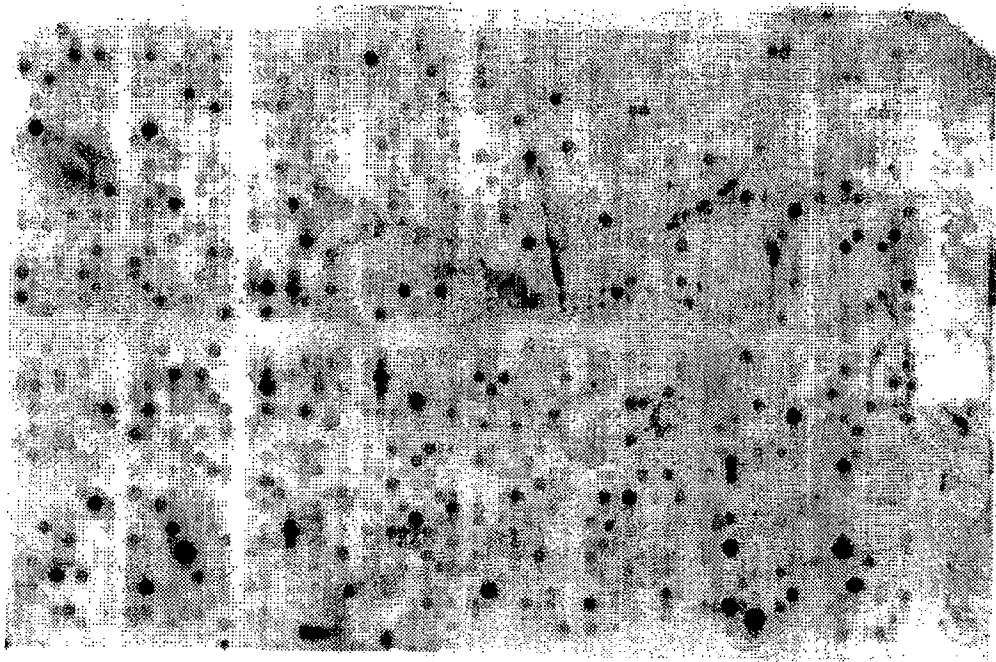
Filter I



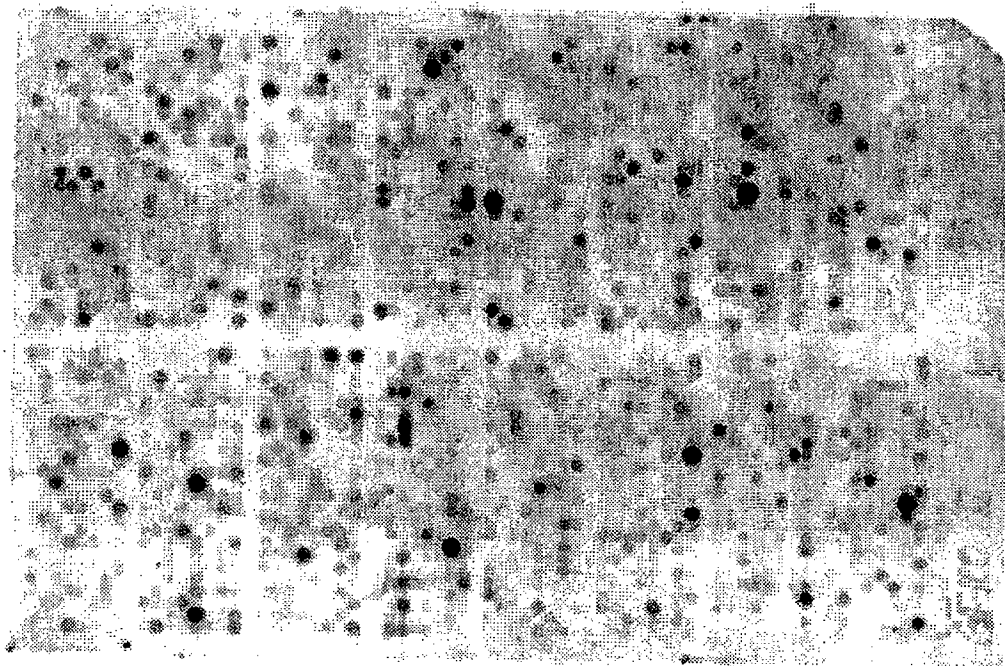
Filter II

FIG. 3A

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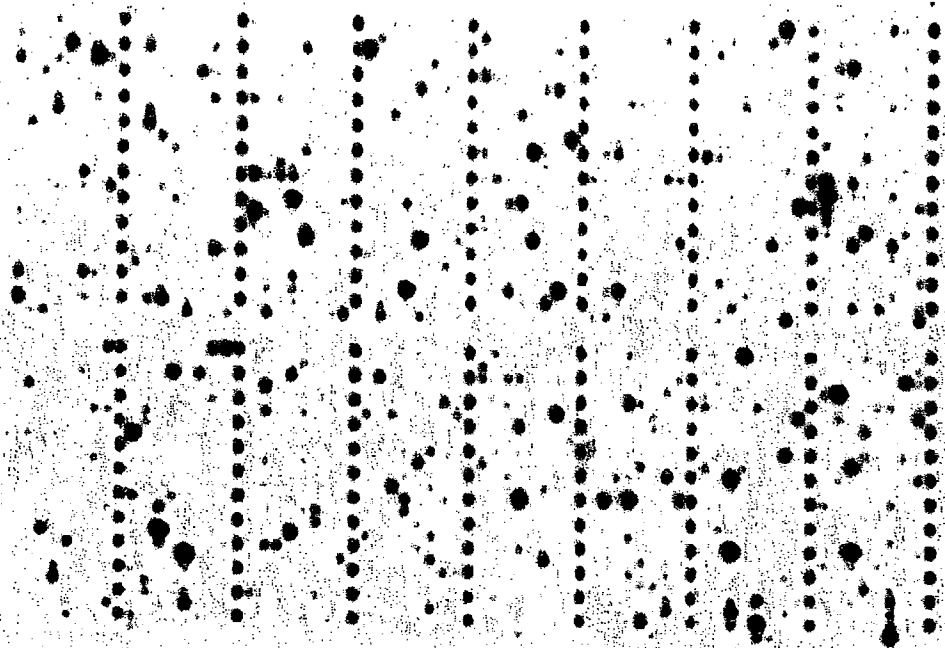
Filter I



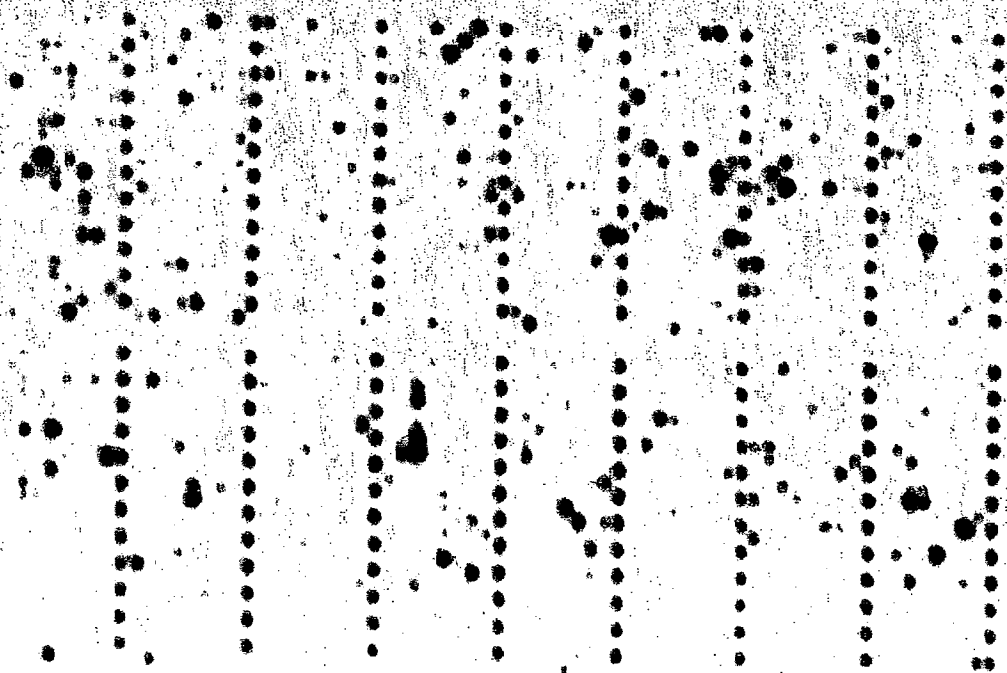
Filter II

FIG. 3B

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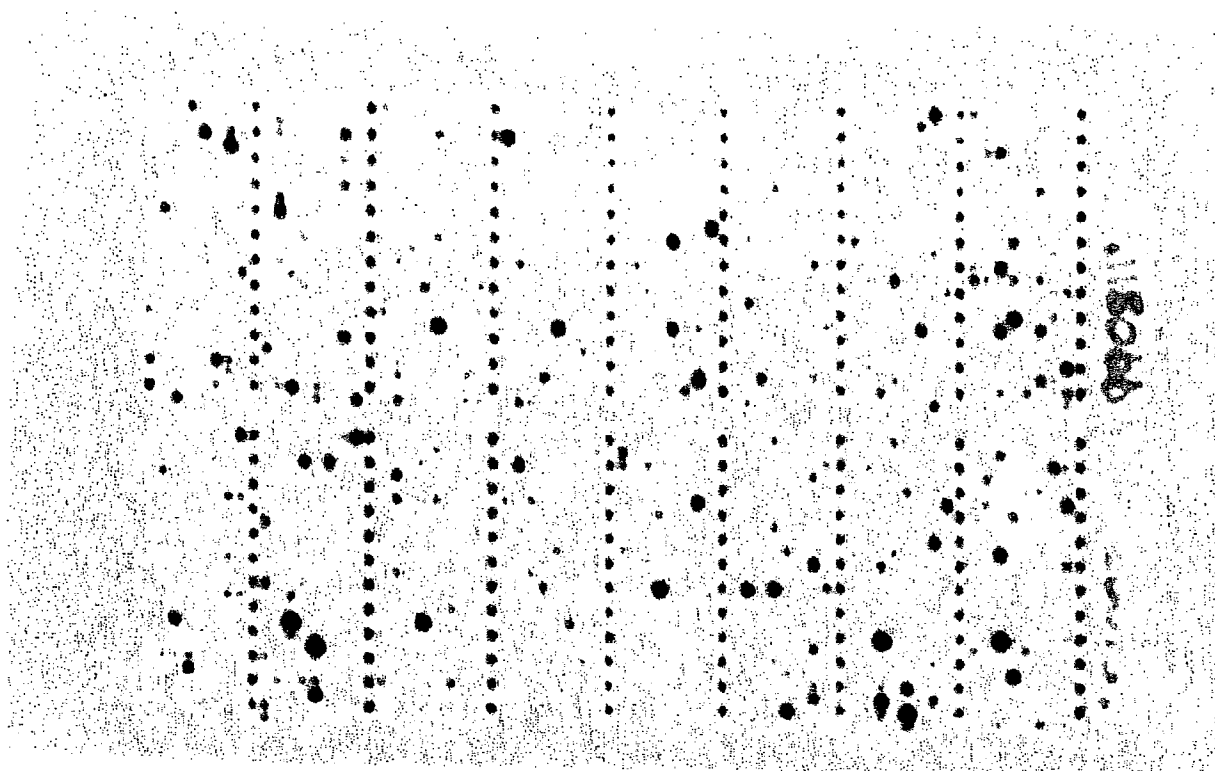
Filter I



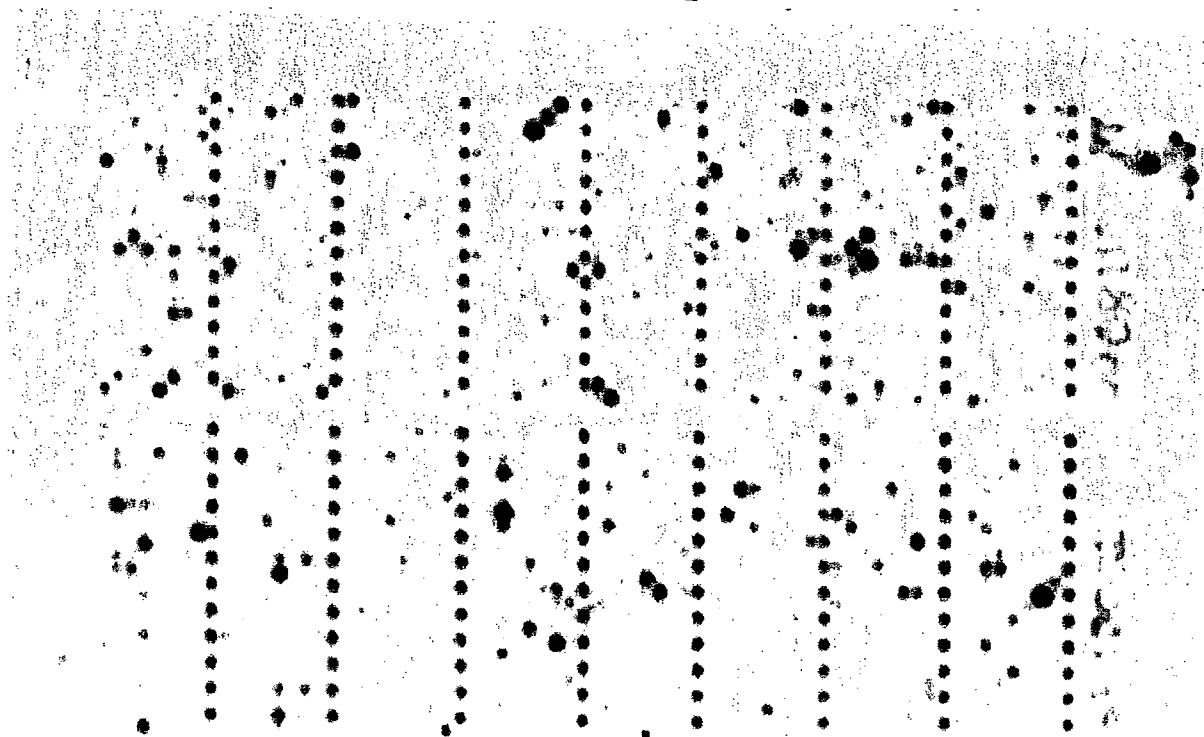
Filter II

FIG. 4A

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Filter I



Filter II

FIG. 4B